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OM protein - protein search, using sw model

Run on: May 20, 2005, 00:24:35 ; Search time 162 Seconds
(without alignments)
229.191 Million cell updates/sec

Title: IIS-10-632-414-3

Perfect score: 514

Sequence: ATTSTGNSARFVNQHLCGSH.....IVEQCCTTSICSLYQLENYCG 96

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 Beq8, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Post-processing: Maximum Match 100%
Listing first 45 summaries

Database : A_GenSeq_16Dec04:*

1: genebeqp1980s:*

2: genebeqp1990s:*

3: genebeqp2000s:*

4: genebeqp2001s:*

5: genebeqp2002s:*

6: genebeqp2003s:*

7: genebeqp2004s:*

8: genebeqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	514	100.0	96	ADN34535
2	508	98.8	8	ADN34534
3	504	98.1	96	ADN34505
4	504	98.1	96	AAO17831
5	504	98.1	97	AAR78661
6	501	97.5	97	AAR78662
7	498	96.9	96	AAU08004
8	498	96.9	96	AAU17830
9	498	96.9	97	ABR68898
10	498	96.9	97	AAW93414
11	497.5	96.8	98	AAV51222
12	497	96.7	99	AAV51223
13	496.5	96.6	100	AAV51224
14	496	96.5	97	AAW93416
15	492	95.7	97	AAW93419
16	492	95.7	97	AAW93415
17	458	89.1	153	AAV53589
18	455	88.5	92	AAR20467
19	455	88.5	93	AAV90102
20	455	88.5	96	ADL24341
21	454	88.3	110	AAPI0042
22	454	88.3	110	AAPI0053
23	454	88.3	110	AAPI40309
24	454	88.3	110	AAV06608
25	454	88.3	110	ADP77582

RESULT 1

ID ADN34535

XX ADN34535

AC ADN34535;

XX DT 17-JUN-2004 (first entry)

DE Preproinsulin peptide fragment #3.

XX KW preproinsulin; insulin; diabetes mellitus; fermentation;

XX genetically modified microorganism.

OS Homo sapiens.

XX PN DEI0235168-A1.

PD 12-FEB-2004.

XX PR 01-AUG-2002; 2002DE-01035168.

PR 01-AUG-2002; 2002DE-01035168.

XX (AVET) AVENTIS PHARMA DEUT GMBH.

XX PI Thurow H, Blumenstock H, Havenith C;

XX DR WPI: 2004-228442/22.

XX PT Purification of preproinsulin, useful for conversion to insulin,

PT comprises removing high molecular weight impurities by anion-exchange

PT then cation-exchange chromatography.

XX PS Claim 3; SEQ ID NO 3; 19pp; German.

XX This invention describes a novel method for purification of preproinsulin which comprises removing high molecular weight substances from an aqueous solution by chromatography on an anion exchanger in flow-through mode and separation by chromatography on a cation exchanger in adsorption mode. A method is also described for preparation of insulin by expression of unfolded preproinsulin. The method is used as part of a process for preparing insulin (for treating diabetes mellitus) by fermentation of genetically modified microorganisms that express unfolded preproinsulin. The method provides efficient removal of contaminants (particularly polymeric preproinsulin) that adversely affect stability of insulin during subsequent processing steps.

XX Sequence 96 AA;

SQ Adf77582 Human ins

Score	Length	DB ID	Description
26	454	88.3	110 3 AAY4367 Human proinsulin
27	454	88.3	110 3 AAY0366 Human ins
28	454	88.3	110 3 ABB26765 Human preproinsulin
29	454	88.3	110 3 AAB06144 Human ins
30	454	88.3	110 4 AAE0337 Human preproinsulin
31	454	88.3	110 4 AAB35424 Secretory insulin
32	454	88.3	110 4 AAG65677 Human proinsulin
33	454	88.3	110 5 ABG60634 Human ins
34	454	88.3	110 5 ABG31590 Human preproinsulin
35	454	88.3	110 6 ABRS5862 Humanised insulin
36	454	88.3	110 6 ADQ9218 Human preproinsulin
37	454	88.3	110 7 ADG56710 Human preproinsulin
38	454	88.3	110 7 ADD6938 Human Proinsulin
39	454	88.3	110 7 ADE7650 Human Proinsulin
40	454	88.3	110 8 ADL25930 Human preproinsulin
41	454	88.3	110 8 ADL24433 Human ins
42	454	88.3	110 8 ADN0699 Human ins
43	454	88.3	110 8 ADL9090 Human ins
44	454	88.3	110 8 ADN49716 Human ins
45	454	88.3	110 8 ADQ14352 Human preproinsulin

ALIGNMENTS

Query Match 100.0%; Score 514; DB 8; Length 96;
 Best Local Similarity 100.0%; Pred. No. 9e-49; Mismatches 0; Indels 0; Gaps 0;
 Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATTSTGNASARFVNQHLCGSHLVEALYLVCGERGFFYPTKTRREADEDPQVQVELGGPQA 60
 Db 1 ATTSTGNASARFVNQHLCGSHLVEALYLVCGERGFFYPTKTRREADEDPQVQVELGGPQA 60

Qy 61 GSLOPLALEGSLOKRGIVEQCCTSTCISLYQLENYC 96
 Db 61 GSLOPLALEGSLOKRGIVEQCCTSTCISLYQLENYC 96

RESULT 2

ADN34534 standard; peptide; 96 AA.
 XX ADN34534;
 AC XX
 DT XX
 DE 17-JUN-2004 (first entry)
 DB XX
 DE Preproinsulin peptide fragment #2.
 KW XX
 KW preproinsulin; insulin; diabetes mellitus; fermentation;
 KW genetically modified microorganism.
 OS Homo sapiens.
 PR DE10235168-A1.
 PN XX
 PD XX
 PT XX
 PR 01-AUG-2002; 2002DE-01035168.
 PR XX
 PR 01-AUG-2002; 2002DE-01035168.
 PA XX
 (AVET) AVENTIS PHARMA DEUT GMBH.
 PA XX
 PT Thurow H, Blumenstock H, Haverinith C;
 PR XX
 PR WPI; 2004-228442/22.

PT purification of preproinsulin, useful for conversion to insulin,
 PT comprises removing high molecular weight impurities by anion-exchange
 PT then cation-exchange chromatography.

PS XX
 PS Claim 2; SEQ ID NO 2; 19pp; German.

XX This invention describes a novel method for purification of preproinsulin
 CC which comprises removing high molecular weight substances from an aqueous
 CC solution by chromatography on an anion exchanger in flow-through mode and
 CC separation by chromatography on a cation exchanger in adsorption mode. A
 CC method is also described for preparation of insulin by expression of
 CC unfolded preproinsulin. The method is used as part of a process for
 CC preparing insulin (for treating diabetes mellitus) by fermentation of
 CC genetically modified microorganisms that express unfolded preproinsulin.
 CC The method provides efficient removal of contaminants (particularly
 CC polymeric preproinsulin) that adversely affect stability of insulin
 XX during subsequent processing steps.

SQ Sequence 96 AA;

Query Match 98.8%; Score 508; DB 8; Length 96;
 Best Local Similarity 100.0%; Pred. No. 4.1e-48; Mismatches 0; Indels 0; Gaps 0;
 Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATTSTGNASARFVNQHLCGSHLVEALYLVCGERGFFYPTKTRREADEDPQVQVELGGPQA 60
 Db 1 ATTSTGNASARFVNQHLCGSHLVEALYLVCGERGFFYPTKTRREADEDPQVQVELGGPQA 60

Qy 61 GSLOPLALEGSLOKRGIVEQCCTSTCISLYQLENYC 95
 Db 61 GSLOPLALEGSLOKRGIVEQCCTSTCISLYQLENYC 95

RESULT 3

ADY08005 standard; peptide; 96 AA.
 AC XX
 DE 08-JUL-1999 (first entry)
 DB XX
 DE Human proinsulin protein fragment 2.
 KW XX
 KW Insulin; human; A chain; B chain; C chain; pro-insulin; chaotropic agent.
 OS Homo sapiens.
 PR XX
 PN XX
 PR 07-APR-1999.
 PR XX
 PR 11-AUG-1998; 98EP-00115048.
 PR XX
 PR 18-AUG-1997; 97DB-01035711.
 PR XX
 PR (HMRI) HOECHST MARION ROUSSEL DEUT GMBH.
 PR XX
 PR Rubroeder FD, Keller R;
 PR XX
 DR WPI; 1999-135401/22.
 PR XX
 PR Preparation of insulin precursors with cystine bridges in the presence of
 PT cysteine and chaotropic auxiliary.
 PR XX
 PR Example 1; Page 12, 16pp; German.
 PR XX
 PR This invention describes a method for the production of insulin or
 CC insulin derivative precursors in an aqueous suspension which are diluted
 CC with cysteine or cysteine hydrochloride to pH 11.5 and then at 55 deg. C
 CC a chaotropic additive is added. This sequence represents human pro-
 CC insulin which is used in the description of the invention. This patent is
 CC an equivalent to RU9801886. (Updated on 20-MAR-2003 to correct DR field.)
 SQ Sequence 96 AA;

Query Match 98.1%; Score 504; DB 2; Length 96;
 Best Local Similarity 99.0%; Pred. No. 1.1e-47; Mismatches 1; Indels 0; Gaps 0;
 Matches 95; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATTSTGNASARFVNQHLCGSHLVEALYLVCGERGFFYPTKTRREADEDPQVQVELGGPQA 60
 Db 1 ATTSTGNASARFVNQHLCGSHLVEALYLVCGERGFFYPTKTRREADEDPQVQVELGGPQA 60

Qy 61 GSLOPLALEGSLOKRGIVEQCCTSTCISLYQLENYC 96
 Db 61 GSLOPLALEGSLOKRGIVEQCCTSTCISLYQLENYC 96

RESULT 4

AA017831 standard; peptide; 96 AA.
 XX AA017831;
 AC XX
 DE 13-SEP-2002 (first entry)
 XX DE Human proinsulin #2.
 KW XX
 KW Human; insulin; cysteine bridge; kaotrophic additive.
 OS Homo sapiens.

XX PR 09-FEB-1995; 95BP-00101748.
 XX PD 23-FEB-2000.
 XX PR 11-AUG-1998; 99BP-00115386.
 XX PR 18-AUG-1997; 97BP-01035711.
 XX PR 11-AUG-1998; 98BP-00115048.
 XX PA (HMR) HOECHST MARION ROUSSEL DEUT GMBH.
 XX PT Rubroeder F, Keller R;
 XX DR WPI; 1999-135401/12.
 PT Preparation of insulin precursors with cystine bridges in the presence of
 cysteine and chaotropic auxiliary.
 PT Example 2, Page 8, 20pp; German.
 XX The present invention relates to insulin or insulin derivative precursors
 in an aqueous suspension, which are diluted with cysteine or cysteine
 hydrochloride to pH 11.5 and then at 55plascC a chaotropic additive is
 added. The present sequence is one version of human proinsulin
 XX sequence 96 AA;
 Query Match 98.1%; Score 504; DB 2; Length 96;
 Best Local Similarity 99.0%; Pred. No. 1.e-47;
 Matches 95; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 CC QY 1 ATTTSGNSARPVNQHLCGSHLVEALVLYCGERGFPTPKTRRAEDPQGVQLGGGGA 60
 CC 1 ATTTSGNSARPVNQHLCGSHLVEALVLYCGERGFPTPKTRRAEDPQGVQLGGGGA 60
 CC Db 61 GS1QPLALEGSLOKRGIVEQCCSICSLYQLENYCG 96
 CC QY 61 GS1QPLALEGSLOKRGIVEQCCSICSLYQLENYCG 96
 CC Do 61 GS1QPLALEGSLOKRGIVEQCCSICSLYQLENYCG 96
 CC
 RESULT 5
 ID AAR78661
 ID AAR78661 standard; protein; 97 AA.
 AC AAR78661;
 XX DT 03-APR-1996 (first entry)
 DE Proinsulin sequence 1.
 XX DE Proinsulin; post-translational modification; recombinant production;
 KW protein folding; conformation.
 OS Synthetic.
 XX PH Key Location/Qualifiers
 Region 1..11
 /label= R1
 /note= "a peptide of 11 amino acids"
 PT Peptide 12..41
 /label= R1-(B2-B29)-Y
 /note= "human insulin B-chain"
 PT Peptide 42..76
 /label= X
 /note= "C-peptide of human insulin"
 PT Peptide 77..97
 /label= R3
 /note= "human insulin A-chain"
 XX PR BP668292-A2.
 XX PD 23-AUG-1995.
 XX DR WPI, 1995-284754/38.
 PS Example 1; Page 7; 16pp; German.
 XX The present sequence is an example of a proinsulin molecule correponding to
 the general formula R2-R1-(B2-B29)-Y-X-Gly-(A2-A20)-R3 (II). In formula
 (II), X = Lys, Arg or a peptide of 2-35 amino acids contg. Lys or Arg at
 the N- and C-terminal; Y = a natural amino acid; R1 = Phe or a bond; R2 =
 H, Arg, Lys, a peptide of 2-45 amino acids contg. Arg or Lys at the N-
 and C-termini; R3 = a natural amino acid; (A2-A20) and (B2-B29) are the
 insulin A- and B-chain sequences from human or other insulin. The
 proinsulin molecule (produced in recombinant E.coli) is reacted with
 mercaptoanil at a ratio of 2-10 SH residues of mercaptoanil per Cys residue of
 proinsulin. The reaction takes place in the presence of a chaotropic
 auxiliary agent at pH 10-11 and results in proinsulin with correctly
 linked cystine bridges. Reaction with trypsin and opt. carboxypeptidase B
 yields correctly folded insulin. The insulin is isolated by absorption on
 CC a hydrophobic resin
 XX SQ Sequence 97 AA;
 Query Match 98.1%; Score 504; DB 2; Length 97;
 Best Local Similarity 99.0%; Pred. No. 1.2e-47;
 Matches 95; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 CC QY 1 ATTTSGNSARPVNQHLCGSHLVEALVLYCGERGFPTPKTRRAEDPQGVQLGGGGA 60
 CC 1 ATTTSGNSARPVNQHLCGSHLVEALVLYCGERGFPTPKTRRAEDPQGVQLGGGGA 60
 CC Db 61 GS1QPLALEGSLOKRGIVEQCCSICSLYQLENYCG 97
 CC QY 61 GS1QPLALEGSLOKRGIVEQCCSICSLYQLENYCG 97
 CC Do 62 GS1QPLALEGSLOKRGIVEQCCSICSLYQLENYCG 97
 CC
 RESULT 6
 ID AAR15472
 ID AAR15472 standard; protein; 97 AA.
 AC AAR15472;
 XX DT 09-JAN-2003 (revised)
 DT 11-MAR-1992 (first entry)
 XX DE Necl-SalI fragment prod. as foreign protein.
 KW Signal peptide; promoter; transcription control; protease; IFN; IL; EGF;
 KW GM-CSF; Factor VIII; insulin; TNF; NGF; vector; foreign protein.
 OS Brevibacillus brevis.
 OS Synthetic.
 PN WO9118101-A.
 XX PD 28-NOV-1991.
 XX PF 11-MAY-1990; 90JP-00122166.
 XX PR 11-MAY-1990; 90JP-00122166.
 PR 30-NOV-1990; 90JP-00334575.
 XX PA (PARH) HOECHST JAPAN LTD.

XX
PI Hashimoto T, Tsujimura A, Udaka J;

XX WI; 1991-36925/50.

DR N-FSDB; AAQ15230.

XX PT Expression vector for signal peptide from *Bacillus brevis* - for expression of interferon, insulin, epidermal growth factor etc. with improved yield.

XX PS Disclosure: Fig 9; 44bp; Japanese.

XX CC DNA encoding the signal peptide associated with the BBR42 gene of *B. brevis* may be incorporated into an expression vector, pref. with the promoter sequence and transcription control region. DNA encoding a foreign protein (e.g. EGF) may be ligated immediately downstream of the signal region. The vector may then be used to transform a host organism which then expresses the protein on culture. BBR42 is secreted by *B. brevis* during an early stage of incubation, and so its associated signal peptide allows a foreign protein to be secreted during this early stage when protease prodn. is low, thus increasing recovery of the protein.

CC Proteins for which the method may be used include interferon,

CC interleukin, human epidermal growth factor, GM-CSF, Factor VIII, insulin, tumour necrosis factor and NGF. See also AAQ15229/31. (Updated on 09-JAN-2003 to add missing OS field.)

XX SQ Sequence 97 AA;

Query Match 97.5%; Score 501; DB 2; Length 97;
Best Local Similarity 98.9%; Pred. No. 2.5e-47; i; Indels 0; Gaps 0;
Matches 94; Conservative 0; Mismatches 1; Del 0; Gaps 0;

QY 1 ATTSTGNSARPVNQHLCGSHLVEALYLVCGERGFFYTPKTRREADPQVQVELGGGPA 60
Db 2 ATTSTGNSARPVNQHLCGSHPBALYLVCGERGFFYTPKTRREADPQVQVELGGGPA 61
QY 61 GSLQPLALEGSIQLKRGIVEQCCTSICSLYQLENYC 95
Db 62 GSLQPLALEGSIQLKRGIVEQCCTSICSLYQLENYC 96

RESULT 8

AAQ17830 standard; peptide; 96 AA.

AC AAQ17830;

XX DT 13 - SSP-2002 (first entry)

DE Human proinsulin #1.

KW Human; insulin; cysteine bridge; chaotropic additive.

OS Homo sapiens.

PN EP0980874-A1.

XX PD 23 - FEB - 2000.

XX PF 11-AUG-1998; 99EP-00115386.

XX PR 18-AUG-1997; 97DE-01035711.

XX PR 11-AUG-1998; 98EP-00115048.

XX PA (HMRI) HOECHST MARION ROUSSEL DEUT GMBH.

XX PI Rubroeder F, Keller R;

XX DR WPI; 1999-135401/12.

XX PS Example 1; Page 6; 20pp; German.

The present invention relates to insulin or insulin derivative precursors in an aqueous suspension, which are diluted with cysteine or cysteine hydrochloride to pH 11.5 and then at 55°C with a chaotropic additive added. The present sequence is one version of human proinsulin

XX SQ Sequence 96 AA;

Query Match 96.9%; Score 498; DB 2; Length 96;
Best Local Similarity 98.9%; Pred. No. 5.2e-47; i; Indels 0; Gaps 0;
Matches 94; Conservative 0; Mismatches 1; Del 0; Gaps 0;

QY 1 ATTSTGNSARPVNQHLCGSHLVEALYLVCGERGFFYTPKTRREADPQVQVELGGGPA 60
Db 1 ATTSTGNSARPVNQHLCGSHLVEALYLVCGERGFFYTPKTRREADPQVQVELGGGPA 60

XX PT Preparation of insulin precursors with cystine bridges in the presence of cysteine and chaotropic auxiliary.

XX PA (HMRI) HOECHST MARION ROUSSEL DEUT GMBH.

XX PI Rubroeder FD, Keller R;

XX DR WPI; 1999-135401/22.

XX PT Preparation of insulin precursors with cystine bridges in the presence of cysteine and chaotropic auxiliary.

Example 1; Page 12; 16pp; German.

XX This invention describes a method for the production of insulin or insulin derivatives precursors in an aqueous suspension which are diluted with cysteine or cysteine hydrochloride to pH 11.5 and then at 55 deg. C with a chaotropic additive is added. This sequence represents human proinsulin which is used in the description of the invention. This patent is an equivalent to HU9801886. (Updated on 20-MAR-2003 to correct DR field.)

XX SQ Sequence 96 AA;

QY	61	GSLOPLALEGSLOQKRGIVEQCCTSCISLYQLENYC	95	AC	AAW93414;
ID	AAR68898	standard; peptide; 97 AA.		XX	DT 11-JUN-1999 (first entry)
Db	61	GSLOPLALEGSLOQKRGIVEQCCTSCISLYQLENYC	95	XX	DE Human insulin derivative peptide #6.
RESULT 9				XX	KW Insulin derivative; human; treatment; diabetes.
AAR68898				XX	OS Synthetic.
ID	AAR68898			OS	Homo sapiens.
XX	AAR68898;			XX	
AC				PN EP85961-A1.	
XX				XX	
DT	25-MAR-2003	(revised)		XX	
DT	02-MAR-1995	{first entry}		PD 23-DEC-1998.	
DE				XX	
XX	Human pro-insulin 1.			PF 15-JUN-1998;	98EP-00110899.
KW	Pro-insulin; A-chain; B-chain; C-chain; disulphide; mercaptan;			PR 20-JUN-1997;	97DE-01026157.
KW	chacropic agent.			XX	
XX				PA (HMRI) HOECHST MARION ROUSSEL DEUT GMBH.	
OS	Homo sapiens.			XX	
XX				PI Ertl J, Habermann P, Geisen K, Seipke G;	
PN	EP600372-A1.			XX	
XX				DR WPI: 1999-047558/05.	
PD	08-JUN-1994.			XX	
XX				PT New fast acting insulin variants - with aminoacid substitutions at	
PP	25-NOV-1993;	93EP-00118993.		PT positions B3, B27, B28 and B29.	
XX				XX	
PR	02-DEC-1992;	92DE-04240420.		PS Claim 38; Page 17-18; 28pp; German.	
XX				XX	
PA	(FARB) HOECHST AG.			CC This invention describes novel fast acting insulin derivatives which have	
XX				CC a Lys residue at position B3 and B27-B29 replaced with another naturally	
PI	Obermeier R, Gerl M, Ludwig J, Sabel W;			CC occurring neutral or acidic amino acid, and with Asn at position A21,	
XX				CC optionally replaced by Asp, Gly, Ser, Thr or Ala, and Phe at position B1,	
DR	WPI: 1994-177718/22.			CC and the amino acid at position B1 are optionally deleted. Such	
XX				CC derivatives can be used for treating diabetes. The derivatives have a	
PT	Prodn. of pro-insulin with correct di:sulphide bridges - by treating			CC faster onset of action than that of wild-type human insulin, especially	
PT	recombinant precursor protein with mercaptan in alkali and in presence of			CC when administered subcutaneously	
XX	chaotropic agent, then isolation on hydrophobic resin.			XX	
PS	Disclosure; Page 10-11; 15pp; German.			SQ Sequence 97 AA;	
XX					
CC	Pro-insulin is produced by treating recombinant precursor protein with a				
CC	mercaptan to provide 2-10 SH residues per Cys residue, in presence of a				
CC	chaotropic agent and in aq. medium of pH 10-11, treating the prod. with 3				
CC	50 g hydrophobic adsorber resin per 1 aq. medium of pH 4-7, isolating				
CC	the adsorbed resin and pro-insulin and desorbing the pro-insulin. This				
CC	method produces pro-insulin with correctly bonded Cys bridges. Compared				
CC	with known methods it involves fewer stages (esp. no sulphitolytic or				
CC	cyanogen bromide cleavage) and overall losses during purification are				
CC	reduced, i.e. the process is quicker and gives better yields. Sequences of pro-				
CC	of insulin chain A, B and C are given in AAW68898-97. Sequences of pro-				
CC	insulin 1-4 are given in AAR68898-901. (Updated on 25-MAR-2003 to correct				
CC	PN field.)				
SQ	Sequence 97 AA;				
Query Match	96.9%	Score 498;	DB 2;	Length 97;	
Best Local Similarity	98.9%	Pred. No. 5.3e-47;			
Matches	94;	Conservative	0;	Mismatches 1;	
Indels	0;	Gaps 0;			
QY	1	ATTSSTGNSARPVNQHLCGSHLVEALYLVCGERGFTPKRRAEDPQVGQVLLGGGA	60	AC AAY51222;	
Db	2	ATTSSTGNSARPVNQHLCGSHLVEALYLVCGERGFTPKRRAEDPQVGQVLLGGGA	61	XX	
QY	61	GSLOPLALEGSLOQKRGIVEQCCTSCISLYQLENYC	95	DT 06-APR-2000 (first entry)	
Db	62	GSLOPLALEGSLOQKRGIVEQCCTSCISLYQLENYC	96	XX	
RESULT 10				DE Human preproinsulin B-chain protein analog His (B0).	
ID	AAW93414	AAW93414 standard; protein; 97 AA.		XX	
XX				KW Inulin; human; antidiabetic; zinc; diabetes mellitus; treatment;	
				KW pharmacodynamic; analog; B chain.	
				XX OS Synthetic.	
				OS Homo sapiens.	
				XX PN DE1982547-A1.	
				PD 09-DEC-1999.	

XX
XX 06-JUN-1998; 98DE-01025447.
PP PT
XX XX
PR XX
XX 06-JUN-1998; 98DE-01025447.
PA DR
PA (HMRI) HOECHST MARION ROUSSEL DEUT GMBH.
XX PT
XX Ertl J, Habermann P, Geisen K, Seipke G, Wollmer A;
XX DR
XX WBI; 2000-098618/09.
PT New insulin analogs and their zinc complexes, with slow onset of
XX activity, for treating diabetes mellitus.
PS Claim 27; Page 18; 22pp; German.
XX
CC This invention describes novel human insulin analogs (I) and their salts,
CC which have antidiabetic activity. (I), also their complexes with zinc,
CC are used for treatment of diabetes mellitus, types I or II. (I) have
CC increased zinc-binding capacity, form stable complexes with zinc and
CC compared with native human insulin have a delayed onset of activity
CC profile, so provide better control of diabetes following subcutaneous
CC injection. Zinc-free formulations do not have slow-release properties, so
CC variation of the zinc content provides control of pharmacodynamics (not
CC possible with native human insulin), e.g. tailored to the requirements of
CC individual patients. This sequence represents a human preproinsulin B
CC chain analog which is used in the method of the invention
XX Sequence 98 AA;

Query Match 96.8%; Score 497.5; DB 3; Length 98;

Best Local Similarity 99.0%; Pred. No. 6 1e-47; 0; Indels 1; Gaps 1;
Matches 95; Conservative 0; Mismatches 1;

Qy 1 ATTSIGNSAR-FNQHQICGSVSHUVEALYLVCGERGFFYTPKTRREADPQVGQVELGGPG 59
Db 2 ATT\$TGN\$ARHFNQHQICGSVSHUVEALYLVCGERGFFYTPKTRREADPQVGQVELGGPG 61

Qy 60 AGSLOPLALEGSIQLQRGIVEQCTSIQLYENYC 95
Db 62 AGSLOPLALEGSIQLQRGIVEQCTSIQLYENYC 97

RESULT 12

AAV5123 ID AAV5123 standard; protein; 99 AA.

AC AAV5123; DT 06-APR-2000 (first entry)
XX Human preproinsulin B-chain protein analog His(B-1).

KW Insulin; human; antidiabetic; zinc; diabetes mellitus; treatment;
XX pharmacodynamic; analog; B chain.

OS Synthetic.
OS Homo sapiens.

XX DE19825447-A1.
DT 06-APR-2000 (first entry)
XX Human preproinsulin B-chain protein analog His(B-1).
XX Insulin; human; antidiabetic; zinc; diabetes mellitus; treatment;
XX pharmacodynamic; analog; B chain.

KW Synthetic.
OS Homo sapiens.

DB19825447-A1.

XX 09-DEC-1999.
XX 09-DEC-1999.

XX 06-JUN-1998; 98DE-01025447.
XX 06-JUN-1998; 98DE-01025447.

XX (HMRI) HOSCHST MARION ROUSSEL DEUT GMBH.
XX PT New insulin analogs and their zinc complexes, with slow onset of
XX activity, for treating diabetes mellitus.

XX PS Claim 29; Page 20; 22pp; German.
XX
CC This invention describes novel human insulin analogs (I) and their salts,
CC which have antidiabetic activity. (I), also their complexes with zinc,
CC are used for treatment of diabetes mellitus, types I or II. (I) have
CC increased zinc-binding capacity, form stable complexes with zinc and
CC compared with native human insulin have a delayed onset of activity
CC profile, so provide better control of diabetes following subcutaneous
CC injection. Zinc-free formulations do not have slow-release properties, so
CC variation of the zinc content provides control of pharmacodynamics (not
CC possible with native human insulin), e.g. tailored to the requirements of
CC individual patients. This sequence represents a human preproinsulin B
CC chain analog which is used in the method of the invention
XX Sequence 99 AA;

Query Match 96.7%; Score 497; DB 3; Length 99;
Best Local Similarity 97.9%; Pred. No. 7e-47; 0; Indels 2; Gaps 1;
Matches 95; Conservative 0; Mismatches 1;

Qy 1 ATTSIGNSAR-FNQHQICGSVSHUVEALYLVCGERGFFYTPKTRREADPQVGQVELGGPG 58
Db 2 ATT\$TGN\$ARHFNQHQICGSVSHUVEALYLVCGERGFFYTPKTRREADPQVGQVELGGPG 61

Qy 59 GAGSLOPLALEGSIQLQRGIVEQCTSIQLYENYC 95
Db 62 GAGSLOPLALEGSIQLQRGIVEQCTSIQLYENYC 98

RESULT 13

AAV51224 ID AAV51224 standard; protein; 100 AA.
XX AC AAV51224;
XX DT 06-APR-2000 (first entry)
XX Human preproinsulin B-chain analog His(B-2), Ala(B-1), Ala(B0).

XX KW Insulin; human; antidiabetic; zinc; diabetes mellitus; treatment;
XX pharmacodynamic; analog; B chain.

OS Synthetic.
OS Homo sapiens.

XX DE19825447-A1.

XX 09-DEC-1999.
XX 06-JUN-1998; 98DE-01025447.

XX 06-JUN-1998; 98DE-01025447.

XX (HMRI) HOECHST MARION ROUSSEL DEUT GMBH.

XX Ertl J, Habermann P, Geisen K, Seipke G, Wollmer A;

XX DR WPI; 2000-098618/09.

XX
CC This invention describes novel human insulin analogs (I) and their salts,
CC which have antidiabetic activity. (I), also their complexes with zinc,
CC are used for treatment of diabetes mellitus, types I or II. (I) have
CC increased zinc-binding capacity, form stable complexes with zinc and
CC compared with native human insulin have a delayed onset of activity
CC profile, so provide better control of diabetes following subcutaneous

CC injection. Zinc-free formulations do not have slow-release properties, so
CC variation of the zinc content provides control of pharmacodynamics (not
CC possible with native human insulin), e.g. tailored to the requirements of
CC individual patients. This sequence represents a human preproinsulin B
CC chain analog which is used in the method of the invention

SQ Sequence 100 AA:

Query Match Similarity 96.6%; Score 496.5; DB 3; Length 100;
Best Local Similarity 96.9%; Pred. No. 8e-47; Mismatches 95; Conservative 0; Indels 0; Gaps 1;
Matches 95; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ATTSTGNSAR--FVNQHLCGSHLVEALYLVCGERGFFYPTKTRREADPQVQVLELGPGAA 57
Db 2 ATTSTGNSARFAFVNQHLCGSHLVEALYLVCGERGFFYPTKTRREADPQVQVLELGPGAA 61

Oy 58 PGAGSILQPLAEGSLQKRGTEQCCSICSLYQLENYC 95
Db 62 PGAGSILQPLAEGSLQKRGTEQCCSICSLYQLENYC 99

RESULT 14

AAW93416 AAW93416 standard; protein; 97 AA.
XX
XX
AC AAW93416;
XX
DT 11-JUN-1999 (first entry)
XX
DE Human insulin derivative peptide #11.
XX
KW Insulin derivative; human; treatment; diabetes.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN BP885961-A1.
XX
PD 23-DEC-1998.
XX
PF 15-JUN-1998; 98BEP-00110889.
XX
PR 20-JUN-1997; 97DE-01026167.
XX
PA (HMBI) HOECHST MARION ROUSSEL DEUT GMBH.
XX
PI Ertl J, Habermann P, Geisen K, Seipke G;
XX
DR WPI; 1999-047558/05.

PT New fast acting insulin variants - with aminoacid substitutions at
PT positions B3, B27, B28 and B29.
XX
PS Claim 37; Page 20-21; 28pp; German.

CC This invention describes novel fast acting insulin derivatives which have
CC a Asn residue at position B3 and B27-B29 replaced with another naturally
CC occurring neutral or acidic amino acid, and with Asn at position A21,
CC optionally replaced by ASP, GLY, Ser, Thr or Ala, and Phe at position B1,
CC and the amino acid at position B1 are optionally deleted. Such
CC derivatives can be used for treating diabetes. The derivatives have a
CC faster onset of action than that of wild-type human insulin, especially
CC when administered subcutaneously
XX
SQ Sequence 97 AA:
Query Match Similarity 95.7%; Score 492; DB 2; Length 97;
Best Local Similarity 97.9%; Pred. No. 2.e-46; Mismatches 93; Conservative 0; Indels 0; Gaps 0;
Matches 93; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ATTSTGNSARFVNQHLCGSHLVEALYLVCGERGFFYPTKTRREADPQVQVLELGPGAA 60
Db 2 ATTSTGNSARFVNQHLCGSHLVEALYLVCGERGFFYPTKTRREADPQVQVLELGPGAA 61

Oy 61 GSLOPLAEGSLQKRGTEQCCSICSLYQLENYC 95
Db 62 GSLOPLAEGSLQKRGTEQCCSICSLYQLENYC 96

PT New fast acting insulin variants - with aminoacid substitutions at
PT positions B3, B27, B28 and B29.
XX
PS Claim 39; Page 19; 28pp; German.

CC This invention describes novel fast acting insulin derivatives which have
CC a Asn residue at position B3 and B27-B29 replaced with another naturally
CC occurring neutral or acidic amino acid, and with Asn at position A21,
CC optionally replaced by ASP, GLY, Ser, Thr or Ala, and Phe at position B1,
CC and the amino acid at position B1 are optionally deleted. Such
CC derivatives can be used for treating diabetes. The derivatives have a
CC faster onset of action than that of wild-type human insulin, especially
CC when administered subcutaneously
XX
SQ Sequence 97 AA;

Query Match Similarity 96.5%; Score 496; DB 2; Length 97;
Best Local Similarity 97.9%; Pred. No. 8.8e-47; Mismatches 93; Conservative 0; Indels 0; Gaps 0;
Matches 93; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ATTSTGNSARFVNQHLCGSHLVEALYLVCGERGFFYPTKTRREADPQVQVLELGPGAA 60
Db 2 ATTSTGNSARFVNQHLCGSHLVEALYLVCGERGFFYPTKTRREADPQVQVLELGPGAA 61

RESULT 15

AAW93419 AAW93419 standard; protein; 97 AA.
XX
AC AAW93419;
XX
DT 11-JUN-1999 (first entry)
XX
DE Human insulin derivative peptide #11.
XX
KW Insulin derivative; human; treatment; diabetes.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN BP885961-A1.

XX
PD 23-DEC-1998.
XX
PF 15-JUN-1998; 98BEP-00110889.
XX
PR 20-JUN-1997; 97DE-01026167.
XX
PA (HMBI) HOECHST MARION ROUSSEL DEUT GMBH.
XX
PI Ertl J, Habermann P, Geisen K, Seipke G;
XX
DR WPI; 1999-047558/05.

PT New fast acting insulin variants - with aminoacid substitutions at
PT positions B3, B27, B28 and B29.
XX
PS Claim 37; Page 20-21; 28pp; German.

CC This invention describes novel fast acting insulin derivatives which have
CC a Asn residue at position B3 and B27-B29 replaced with another naturally
CC occurring neutral or acidic amino acid, and with Asn at position A21,
CC optionally replaced by ASP, GLY, Ser, Thr or Ala, and Phe at position B1,
CC and the amino acid at position B1 are optionally deleted. Such
CC derivatives can be used for treating diabetes. The derivatives have a
CC faster onset of action than that of wild-type human insulin, especially
CC when administered subcutaneously
XX
SQ Sequence 97 AA:

Query Match Similarity 95.7%; Score 492; DB 2; Length 97;
Best Local Similarity 97.9%; Pred. No. 2.e-46; Mismatches 93; Conservative 0; Indels 0; Gaps 0;
Matches 93; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ATTSTGNSARFVNQHLCGSHLVEALYLVCGERGFFYPTKTRREADPQVQVLELGPGAA 60
Db 2 ATTSTGNSARFVNQHLCGSHLVEALYLVCGERGFFYPTKTRREADPQVQVLELGPGAA 61

Oy 61 GSLOPLAEGSLQKRGTEQCCSICSLYQLENYC 95
Db 62 GSLOPLAEGSLQKRGTEQCCSICSLYQLENYC 96

Search completed: May 20, 2005, 00:41:40
Job time : 166 secs

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GenCore version 5.1.6
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Om protein - protein search, using sw model

Run on:

May 20, 2005, 00:36:01 ; Search time 43 Seconds

(Without alignments)

166.658 Million cell updates/sec

Title: US-10-632-414-3
Perfect score: 514
Sequence: 1. ATTSGNSARFVNQHLCGSH..... IVEQQCTSTICSLYQLENYCG 96

Scoring table: BLOSUM62
GapOp 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: 'Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/pctdata/l1/aa/5A_COMB.pep:*
- 2: /cgn2_6/pctdata/l1/aa/5B_COMB.pep:*
- 3: /cgn2_6/pctdata/l1/aa/6A_COMB.pep:*
- 4: /cgn2_6/pctdata/l1/aa/6B_COMB.pep:*
- 5: /cgn2_6/pctdata/l1/aa/POTUS_COMB.pep:*
- 6: /cgn2_6/pctdata/l1/aa/backfillsl.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

* Query

Result No.

Score

Query Length

DB ID

Description

Result No.	Score	Query Length	DB ID	Description
1	504	98.1	96	2 US-09-134-834-5
2	504	98.1	96	3 US-09-386-303A-5
3	504	98.1	96	4 US-09-947-553-5
4	504	98.1	97	1 US-08-389-487-4
5	498	96.9	96	2 US-09-134-833-6
6	498	96.9	96	3 US-09-386-303A-4
7	498	96.9	96	4 US-09-947-553-4
8	498	96.9	97	1 US-09-160-376A-4
9	498	96.9	97	3 US-09-099-307-5
10	497.5	96.8	98	4 US-09-701-968-8
11	497	96.7	99	4 US-09-701-968-8
12	496.5	96.6	100	4 US-09-701-968-9
13	496	96.5	97	3 US-09-099-307-8
14	492	95.7	97	3 US-09-099-307-7
15	492	95.7	97	3 US-09-099-307-11
16	497	93.2	90	1 US-08-030-731A-43
17	454	88.3	110	3 US-08-950-720A-11
18	454	88.3	110	3 US-08-589-028-2
19	454	88.3	110	3 US-08-784-58B-2
20	454	88.3	110	3 US-08-785-271-2
21	454	88.3	110	4 US-08-472-701-2
22	454	88.3	110	4 US-08-185-852-2
23	454	88.3	110	4 US-09-815-229-3
24	454	88.3	110	4 US-09-617-389B-20
25	454	88.3	110	4 US-09-323-738-2
26	454	88.3	110	4 US-09-015-399-7
27	88.3	110	4 US-09-015-399-7	

ALIGNMENTS

RESULT 1	US-09-134-836-5
Sequence	5, Application US/09134836
Patent No.	5986048
GENERAL INFORMATION:	
APPLICANT:	Rubroder, Franz-Josef
INVENTOR:	Keller, Reinhold
TITLE OF INVENTION:	Improved process for obtaining insulin precursors having correctly bonded cysteine bridges
NUMBER OF SEQUENCES:	7
CORRESPONDENCE ADDRESS:	
ADDRESSEE:	Finnegan, Henderson, Farrabow, Garrett & Dunner
STREET:	1300 I Street, N.W.
CITY:	Washington
STATE:	D.C.
COUNTRY:	USA
ZIP:	20005-3315
COMPUTER READABLE FORM:	
MEDIUM TYPE:	Floppy disk
COMPUTER:	IBM PC compatible
OPERATING SYSTEM:	PC-DOS/MS-DOS
SOFTWARE:	Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:	
APPLICATION NUMBER:	US/09-134-836
FILING DATE:	
CLASSIFICATION:	
ATTORNEY/AGENT INFORMATION:	
NAME:	Leisl McDonald
REGISTRATION NUMBER:	34-872
REFERENCE/DOCKET NUMBER:	02481-1600-00000
TELECOMMUNICATION INFORMATION:	
TELEPHONE:	(202) 408-4400
TELEFAX:	(202) 408-4400
INFORMATION FOR SEQ ID NO:	5:
SEQUENCE CHARACTERISTICS:	
LENGTH:	96 amino acids
TYPE:	amino acid
STRANDEDNESS:	single
TOPOLOGY:	linear
MOLECULE TYPE:	protein
ORIGINAL SOURCE:	
ORGANISM:	Escherichia coli
FEATURE:	
NAME/KEY:	Protein
LOCATION:	1..96
US-09-134-836-5	
Query Match	98.1%
Best Local Similarity	99.0%
PCT-US95-08596-2	
Length	96;

Matches 95; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 61 GSLQPLALEGSLOKRGIVEQCCTSCSLYOLENYCG 96

Qy 1 ATTSTGNSARFVNQHLCGSHLVEALYLVCGERGFFYPTKTRREADLQVQVELGGGPGA 60

Db 1 ATTSTGNSARFVNQHLCGSHLVEALYLVCGERGFFYPTKTRREADLQVQVELGGGPGA 60

Qy 61 GSLQPLALEGSLOKRGIVEQCCTSCSLYOLENYCG 96

Db 61 GSLQPLALEGSLOKRGIVEQCCTSCSLYOLENYCG 96

RESULT 2

US-09-386-303A-5

; Sequence 5, Application US/09386303A

; Patent No. 6380355

; GENERAL INFORMATION:

; APPLICANT: Rubroder, Franz-Josef

; ; Keller, Reinhold

TITLE OF INVENTION: Improved process for obtaining insulin precursors having correctly bonded cystine bridges

NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS:

ADRESSEE: Finnegans, Henderson, Farrabow, Garrett & Dunner

STREET: 1300 I Street, N.W.

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20005-3315

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/386,303A

FILING DATE: 31-Aug-1999

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/134,836

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Leslie McDonell

REGISTRATION NUMBER: 34,872

REFERENCE/DOCKET NUMBER: 02481.1600-00000

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 408-4400

TELEFAX: (202) 408-4400

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 96 amino acids

TYPE: amino acid

STRANDEDNESS: Single

TOPOLOGY: linear

MOLECULE TYPE: Protein

MOLECULE SOURCE:

ORGANISM: Escherichia coli

FEATURE:

NAME/KEY: Protein

LOCATION: 1..96

SEQUENCE DESCRIPTION: SEQ ID NO: 5:

US-09-386-303A-5

Query Match 98.1%; Score 504; DB 3; Length 96;

Best Local Similarity 99.0%; Pred. No. 7.7e-52; 1; Indels 0; Gaps 0;

Matches 95; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATTSTGNSARFVNQHLCGSHLVEALYLVCGERGFFYPTKTRREADLQVQVELGGGPGA 60

Db 1 ATTSTGNSARFVNQHLCGSHLVEALYLVCGERGFFYPTKTRREADLQVQVELGGGPGA 60

Qy 61 GSLQPLALEGSLOKRGIVEQCCTSCSLYOLENYCG 96

Db 61 GSLQPLALEGSLOKRGIVEQCCTSCSLYOLENYCG 96

RESULT 4

US-08-389-487-7

; Sequence 7, Application US/08389487

; Patent No. 563291

; GENERAL INFORMATION:

APPLICANT: Obermeier, Rainer
 APPLICANT: Gerl, Martin
 APPLICANT: Ludwig, Jurgen
 APPLICANT: Sabel, Walter
 TITLE OF INVENTION: Process for Obtaining Insulin Having Correctly Linked Cystine Bridges
 NUMBER OF SEQUENCES: 12
 CORRESPONDENCE ADDRESS: Finnegans, Henderson, Farrabow, Garrett & Dunner
 COUNTRY: United States of America
 ZIP: 20005-3315
 COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/389,487
 FILING DATE:
 CLASSIFICATION: 530
 ATTORNEY/AGENT INFORMATION:
 NAME: Binaudi, Carol P.
 REGISTRATION NUMBER: 32,220
 REFERENCE/DOCKET NUMBER: 02481.1424-00000
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-408-4400
 TELEFAX: (202) 408-4400
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 97 amino acids
 TYPE: amino acid
 STRANDEDNESS: Single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 ORIGINAL SOURCE:
 ORGANISM: Escherichia coli
 FEATURE:
 NAME/KEY: Protein
 LOCATION: 1..96
 US-09-134-836-4

Query Match 98.1%; Score 504; DB 1; Length 97;
 Best Local Similarity 99.0%; Pred. No. 7.8e-52; Mismatches 1; Indels 0; Gaps 0;
 Matches 95; Conservative 0; MisMatches 1; Indels 0; Gaps 0;

Qy 1 ATTSTGNSARFVNQHLCGSHLVEALYLVCGERGFPTPKTRREADLQVQVELGGGPA 60
 Db 2 ATTSTGNSARFVNQHLCGSHLVEALYLVCGERGFPTPKTRREADLQVQVELGGGPA 61

Query Match 96.9%; Score 498; DB 2; Length 95;
 Best Local Similarity 98.9%; Pred. No. 3.9e-51; Mismatches 1; Indels 0; Gaps 0;
 Matches 94; Conservative 0; MisMatches 1; Indels 0; Gaps 0;

Qy 1 ATTSTGNSARFVNQHLCGSHLVEALYLVCGERGFPTPKTRREADLQVQVELGGGPA 60
 Db 1 ATTSTGNSARFVNQHLCGSHLVEALYLVCGERGFPTPKTRREADLQVQVELGGGPA 60

Query Match 96.9%; Score 498; DB 2; Length 95;
 Best Local Similarity 98.9%; Pred. No. 3.9e-51; Mismatches 1; Indels 0; Gaps 0;
 Matches 94; Conservative 0; MisMatches 1; Indels 0; Gaps 0;

Qy 61 GSLOPLAEGSLSQKRGIVEQCCSTSICSLYOLENYCG 96
 Db 62 GSLOPLAEGSLSQKRGIVEQCCSTSICSLYOLENYCG 97

RESULT 5
 US-09-134-836-4
 Sequence 4, Application US/09134836
 Patent No. 598608
 GENERAL INFORMATION:
 APPLICANT: Rubroder, Franz-Josef
 APPLICANT: Rubroder, Franz-Josef
 APPLICANT: Keller, Reinhold
 TITLE OF INVENTION: Improved process for obtaining insulin precursors having correctly bonded cystine bridges
 NUMBER OF SEQUENCES: 7
 CORRESPONDENCE ADDRESS:
 ADDRESSE: Finnegans, Henderson, Farrabow, Garrett & Dunner
 STREET: 1300 I Street, N.W.
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20005-3315
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/316,303A
 FILING DATE: 31-Aug-1999
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/134,836
 FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Leslie McDonell

REGISTRATION NUMBER: 34,872
 TELECOMMUNICATION/DOCKET NUMBER: 02481.1600-00000
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 96 amino acids
 STRANDEDNESS: single
 MOLECULE TYPE: protein
 ORIGINAL SOURCE:
 NAME/KEY: Protein
 LOCATION: 1..96
 SEQUENCE DESCRIPTION: SEQ ID NO: 4:
 US-09-386-303A-4

Query Match 96.9%; Score 498; DB 3; Length 96;
 Best Local Similarity 98.9%; Pred. No. 3.9e-51;
 Matches 94; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATTSTGNARSFVNQHLCGSHLVEALYLVCGERGFFYTPKTRREADLQVQVELGGGGA 60
 1 ATTSTGNARSFVNQHLCGSHLVEALYLVCGERGFFYTPKTRREADLQVQVELGGGGA 60

Qy 61 GSLQPLALEGSLQKRGIVEQCCTSCISLYQLENYC 95
 61 GSLQPLALEGSLQKRGIVEQCCTSCISLYQLENYC 95

Db 61 GSLQPLALEGSLQKRGIVEQCCTSCISLYQLENYC 95

RESULT 7

; Sequence 4, Application US/09947563
 ; Patent No. 6,227,346

; GENERAL INFORMATION:
 APPLICANT: Rubroder, Franz-Josef
 Kehler, Reinhold

; TITLE OF INVENTION: Improved processes for obtaining correctly bonded cystine bridges in builn precursors having correctly bonded cystine bridges

; NUMBER OF SEQUENCES: 7

; CORRESPONDENCE ADDRESS:
 ADDRESSEE: Finnegan, Henderson, Parrabow, Garrett & Dunner
 STREET: 1300 I Street, N.W.
 CITY: Washington
 STATE: D.C.
 ZIP: 20005-3315

; COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS

; CURRENT APPLICATION DATA:
 CURRENT APPLICATION NUMBER: US/09/947,563
 FILING DATE: 07-sep-2001
 CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/134,836
 FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Leslie McDonell
 REGISTRATION NUMBER: 34,872
 REFERENCE/DOCKET NUMBER: 02481.1600-00000
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 408-4400
 TELEFAX: (202) 408-4400

INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 96 amino acids

Query Match 96.9%; Score 498; DB 1; Length 97;
 Best Local Similarity 98.9%; Pred. No. 3.9e-51;

RESULT 8

; Sequence 4, Application US/08160376A
 ; Patent No. 5,730,949

; GENERAL INFORMATION:
 APPLICANT: Obermeier, Ranier
 APPLICANT: Gerl, Martin
 APPLICANT: Ludwig, Jurgen

; TITLE OF INVENTION: Process For Obtaining Proinsulin Possessing Correctly Linked Cystine Bridges

; NUMBER OF SEQUENCES: 7

; CORRESPONDENCE ADDRESS:
 ADDRESSEE: Kenneth A. Genoni, Esq.
 STREET: Rt. 202-206 No. 5473049th/P.O. Box 2500
 CITY: Somerville
 STATE: New Jersey
 COUNTRY: U.S.A.
 ZIP: 08876-1258

; COMPUTER READABLE FORM:
 MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
 COMPUTER: IBM 386
 OPERATING SYSTEM: WINDOWS 3.1
 SOFTWARE: WORDPERFECT 5.1

; CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/160,376A
 FILING DATE: December 1, 1993
 CLASSIFICATION: 530

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: GR P 4240420-7
 FILING DATE: December 2, 1992

ATTORNEY/AGENT INFORMATION:
 NAME: Barbara V. Maurer, Esq.
 REGISTRATION NUMBER: 31,287
 REFERENCE/DOCKET NUMBER: HOE 92/F 384

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (908) 231-4079
 TELEFAX: (908) 231-2555

INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 97 Amino Acids
 TYPE: Amino Acid (AA)
 TOPOLOGY: not relevant

US-08-160-376A-4

RESULT 9
US-09-099-307-6
; Sequence 6, Application US/09099307A
; Patent No. 6221633
; GENERAL INFORMATION:
; APPLICANT: ERTL, JOHANN
; APPLICANT: HABERMANN, PAUL
; APPLICANT: GEISEN, KARL
; APPLICANT: SEIPKE, GERHARD
; TITLE OF INVENTION: NOVEL INSULIN DERIVATIVES HAVING A RAPID ONSET OF ACTION
; FILE REFERENCE: 02481.1597-00000
; CURRENT APPLICATION NUMBER: US/09/099, 307A
; CURRENT FILING DATE: 1998-06-18
; EARLIER FILING DATE: 1997-06-20
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 6
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-099-307-6

Query Match 96.9%; Score 498; DB 3; Length 97;
Best Local Similarity 97.9%; Pred. No. 3.9e-51; Mismatches 1; Indels 0; Gaps 0;
Matches 93; Conservative 1; MisMatches 1; Indels 0; Gaps 0;

Qy 1 ATTSTGNNSARPNQHQLCGSHLVEALYLVCGERGFFYTPKTRREAEDPQVQVELGGP 60
Db 2 ATTSTGNNSARPKHQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDPQVQVELGGP 61

Qy 61 GSLOPLALEGSLOKRQGIVEQCCSISLYQLENYC 95
Db 62 GSLOPLALEGSLOKRQGIVEQCCSISLYQLENYC 96

RESULT 10
US-09-701-968-7
; Sequence 7, Application US/09701968
; Patent No. 6686177
; GENERAL INFORMATION:
; APPLICANT: ERTL, JOHANN
; APPLICANT: HABERMANN, PAUL
; APPLICANT: GEISEN, KARL
; APPLICANT: SEIPKE, GERHARD
; TITLE OF INVENTION: NOVEL INSULIN ANALOGS WITH ENHANCED ZINC BINDING
; FILE REFERENCE: 02481.1719-00000
; CURRENT APPLICATION NUMBER: US/09/701, 968
; CURRENT FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 7
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-701-968-7

Query Match 96.9%; Score 497.5; DB 4; Length 98;
Best Local Similarity 99.0%; Pred. No. 4.6e-51; Mismatches 0; Indels 1; Gaps 1;
Matches 95; Conservative 0; MisMatches 0; Indels 1; Gaps 1;

Qy 1 ATTSTGNNSARPNQHQLCGSHLVEALYLVCGERGFFYTPKTRREAEDPQVQVELGGP 59
Db 2 ATTSTGNNSARPKHQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDPQVQVELGGP 61

RESULT 11
US-09-701-968-8
; Sequence 8, Application US/09701968
; Patent No. 6686177
; GENERAL INFORMATION:
; APPLICANT: ERTL, JOHANN
; APPLICANT: HABERMANN, PAUL
; APPLICANT: GEISEN, KARL
; APPLICANT: SEIPKE, GERHARD
; APPLICANT: WOLLMER, AXEL
; TITLE OF INVENTION: NOVEL INSULIN ANALOGS WITH ENHANCED ZINC BINDING
; FILE REFERENCE: 02481.1719-00000
; CURRENT APPLICATION NUMBER: US/09/701, 968
; CURRENT FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 8
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-701-968-8

Query Match 96.7%; Score 497; DB 4; Length 99;
Best Local Similarity 97.9%; Pred. No. 5.3e-51; Mismatches 0; Indels 2; Gaps 1;
Matches 95; Conservative 0; MisMatches 0; Indels 2; Gaps 1;

Qy 1 ATTSTGNNSAR--FNQHQLCGSHLVEALYLVCGERGFFYTPKTRREAEDPQVQVELGGP 58
Db 2 ATTSTGNNSARHAFNQHQLCGSHLVEALYLVCGERGFFYTPKTRREAEDPQVQVELGGP 61

Qy 59 GAGSIQPLALEGSLOKRQGIVEQCCSISLYQLENYC 95
Db 62 GAGSIQPLALEGSLOKRQGIVEQCCSISLYQLENYC 98

RESULT 12
US-09-701-968-9
; Sequence 9, Application US/09701968
; Patent No. 6686177
; GENERAL INFORMATION:
; APPLICANT: ERTL, JOHANN
; APPLICANT: HABERMANN, PAUL
; APPLICANT: GEISEN, KARL
; APPLICANT: SEIPKE, GERHARD
; APPLICANT: WOLLMER, AXEL
; TITLE OF INVENTION: NOVEL INSULIN ANALOGS WITH ENHANCED ZINC BINDING
; FILE REFERENCE: 02481.1719-00000
; CURRENT APPLICATION NUMBER: US/09/701, 968
; CURRENT FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 9
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-701-968-9

Query Match 95.6%; Score 496.5; DB 4; Length 100;
Best Local Similarity 96.9%; Pred. No. 6.2e-51; Mismatches 0; Indels 3; Gaps 1;

Qy 1 ATTSTGNNSAR--FNQHQLCGSHLVEALYLVCGERGFFYTPKTRREAEDPQVQVELGGP 57
Db 2 ATTSTGNNSARHAFNQHQLCGSHLVEALYLVCGERGFFYTPKTRREAEDPQVQVELGGP 61

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RESULT 13
US-09-099-307-8
; Sequence 8, Application US/09099307A
; Patent No. 6221633
; GENERAL INFORMATION:
; APPLICANT: ERTL, JOHANN
; APPLICANT: HABERMANN, PAUL
; APPLICANT: GEISEN, KARL
; APPLICANT: SELPE, GERHARD
; TITLE OF INVENTION: NOVEL INSULIN DERIVATIVES HAVING A RAPID ONSET OF ACTION
; FILE REFERENCE: 02481.1597-00000
; CURRENT APPLICATION NUMBER: US/09/099, 307A
; CURRENT FILING DATE: 1998-06-18
; EARLIER APPLICATION NUMBER: 19726167.1
; EARLIER FILING DATE: 1997-06-20
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 8
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-099-307-8

RESULT 14
US 09-099-307-7
; Sequence 7, Application US/09099307A
; Patent No. 6221633
; GENERAL INFORMATION:
; APPLICANT: ERTL, JOHANN
; APPLICANT: HABERMANN, PAUL
; APPLICANT: GEISEN, KARL
; APPLICANT: SELPE, GERHARD
; TITLE OF INVENTION: NOVEL INSULIN DERIVATIVES HAVING A RAPID ONSET OF ACTION
; FILE REFERENCE: 02481.1597-00000
; CURRENT APPLICATION NUMBER: US/09/099, 307A
; CURRENT FILING DATE: 1998-06-18
; EARLIER APPLICATION NUMBER: 19726167.1
; EARLIER FILING DATE: 1997-06-20
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 11
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-099-307-11
; US-09-099-307-11

RESULT 15
US-09-099-307-11
; Sequence 11, Application US/09099307A
; Patent No. 6221633
; GENERAL INFORMATION:
; APPLICANT: ERTL, JOHANN
; APPLICANT: HABERMANN, PAUL
; APPLICANT: GEISEN, KARL
; APPLICANT: SELPE, GERHARD
; TITLE OF INVENTION: NOVEL INSULIN DERIVATIVES HAVING A RAPID ONSET OF ACTION
; FILE REFERENCE: 02481.1597-00000
; CURRENT APPLICATION NUMBER: US/09/099, 307A
; CURRENT FILING DATE: 1998-06-18
; EARLIER APPLICATION NUMBER: 19726167.1
; EARLIER FILING DATE: 1997-06-20
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 11
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-099-307-11

Query Match 95.7%; Score 492; DB 3; Length 97;
Best Local Similarity 97.9%; Pred. No. 6-8e-51; Matches 93; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Db 2 ATSTGNARSARFVNQHLCGSHLVEALYLGCGERGRGFTPKTRREADPQVQVELGGGGA 61
Query 61 GSLOPLALEGSLOQKRGIVEQCCTSCISLYOLENYC 95
Db 62 GSLOPLALEGSLOQKRGIVEQCCTSCISLYOLENYC 96

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Job time : 45 secs

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Om protein - protein search, using sw model

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Title: US-10-632-414-3

Perfect score: 514

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Maximum Match 100%

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 19: /cgn2_6/ptodata/2/pubpaa/us60_PUBCOMB.pep: *
 /cgn2_6/ptodata/2/pubpaa/us60_PUBCOMB.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	508	98.8	96	17 US-10-632-414-2
3	504	98.1	96	9 US-09-947-563-5
4	498	96.9	9	US-09-947-563-4
5	460	89.5	110	17 US-10-869-040-21
6	460	89.5	110	17 US-10-869-040-22
7	456	88.7	257	17 US-10-869-040-196
8	454	88.3	110	9 US-09-205-658-125
9	454	88.3	110	9 US-09-815-229-3
10	454	88.3	110	9 US-09-804-409A-9
11	454	88.3	110	10 US-09-965-748C-6
12	454	88.3	110	10 US-09-965-748C-125
13	454	88.3	110	14 US-10-038-686-1

score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

RESULT 2
US-10-632-414-2
Sequence 2, Application US/10632414
; Publication No. US2005008000A1
; GENERAL INFORMATION:
; APPLICANT: Aventis Pharma Deutschland GmbH
; APPLICANT: THURW, Horst
; APPLICANT: BLUMENSTOCK, Hans
; APPLICANT: HAVENTH, Chantal
; APPLICANT: ERTL, Johann
TITLE OF INVENTION: A METHOD FOR PURIFYING PREPROINSULIN
CURRENT APPLICATION NUMBER: US/10/632,414
FILE REFERENCE: DAV2002/0053 US NP
CURRENT FILING DATE: 2003-08-01
PRIORITY FILING DATE: 2002-12-16
PRIORITY APPLICATION NUMBER: DE10235168, 6
PRIORITY FILING DATE: 2002-08-01
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 96
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Preproinsulin I
Query Match 98.8%; Score 508; DB 17; Length 96;
Best Local Similarity 100.0%; Pred. No. 2.1e-48;
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATTSIGNSARVNQHQICGSHLVEALYLVCGERGFFTPKTRRAEDPQVQVELGGPG 60
Db 1 ATTSGNSARTVNQHQICGSHLVEALYLVCGERGFFTPKTRRAEDPQVQVELGGPG 60
QY 61 GSLQPIALEGSLSQKRGIVEOQCTSCISLYOLENYC 95
Db 61 GSLQPIALEGSLSQKRGIVEOQCTSCISLYOLENYC 95

RESULT 3
US-09-947-563-5
; Sequence 5, Application US/09947563
; Patent No. US20050156234A1
; GENERAL INFORMATION:
; APPLICANT: Rubroder, Franz-Josef
; TITLE OF INVENTION: Improved process for obtaining
NUMBER OF SEQUENCES: 7 insulin precursors having correctly bonded cystine bridges
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farrabow, Garrett & Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.3.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/947,563
; FILING DATE: 07-Sep-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/134,836
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Leslie McDonell
; REGISTRATION NUMBER: 34,872
; REFERENCE/DOCKET NUMBER: 02481.1600-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-0000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 96 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Escherichia coli
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..96
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
; US-09-947-563-5
; Query Match 98.1%; Score 504; DB 9; Length 96;
; Best Local Similarity 99.0%; Pred. No. 5.7e-48;
; Matches 95; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
; QY 1 ATTSIGNSARVNQHQICGSHLVEALYLVCGERGFFTPKTRRAEDPQVQVELGGPG 60
; Db 1 ATTSGNSARTVNQHQICGSHLVEALYLVCGERGFFTPKTRRAEDPQVQVELGGPG 60
; QY 61 GSLQPIALEGSLSQKRGIVEOQCTSCISLYOLENYC 96
; Db 61 GSLQPIALEGSLSQKRGIVEOQCTSCISLYOLENYC 96

RESULT 4
US-09-947-563-4
; Sequence 4, Application US/09947563
; Patent No. US20050156234A1
; GENERAL INFORMATION:
; APPLICANT: Rubroder, Franz-Josef
; TITLE OF INVENTION: Improved process for obtaining
NUMBER OF SEQUENCES: 7 insulin precursors having correctly bonded cystine bridges
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farrabow, Garrett & Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.3.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/947,563
; FILING DATE: 07-Sep-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/134,836
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Leslie McDonell
; REGISTRATION NUMBER: 34,872
; REFERENCE/DOCKET NUMBER: 02481.1600-00000


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Db      |||||||LQPLALEGSLOKRGIVEQCCTCSLYQLENYC 256
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; Sequence 125, Application US/09205658
; Patent No. US20010029617A1
; GENERAL INFORMATION:
; APPLICANT: Rivkun, Gary
; APPLICANT: Osg, Scott
; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR
; TITLE OF INVENTION: IMPAIRED GLUCOSE TOLERANCE CONDITIONS
; FILE REFERENCE: 00786/351004
; CURRENT APPLICATION NUMBER: US/09/205, 658
; CURRENT FILING DATE: 1998-12-03
; EARLIER APPLICATION NUMBER: 08/857, 076
; EARLIER FILING DATE: 1997-05-15
; EARLIER APPLICATION NUMBER: 08/888, 534
; EARLIER FILING DATE: 1997-07-07
; EARLIER APPLICATION NUMBER: US98/10080
; EARLIER FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 328
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 125
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-205-658-125

Query Match          88.3%; Score 454; DB 9; Length 110;
Best Local Similarity 96.6%; Pred. No. 2.3e-42; Indels 0; Gaps 0;
Matches 85; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy      8 SARPVNQHICSHLVEALYLVCGERGFYPTKTRREADPQVQVELGGGAGS1QPLA 67
Db      22 AAFAVNQHLCGSHLVEALYLVCGERGFYPTKTRREADPQVQVELGGGAGS1QPLA 81

Query Match          88.3%; Score 454; DB 9; Length 110;
Best Local Similarity 96.6%; Pred. No. 2.3e-42; Indels 0; Gaps 0;
Matches 85; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy      8 SARPVNQHICSHLVEALYLVCGERGFYPTKTRREADPQVQVELGGGAGS1QPLA 67
Db      82 LEGSLQKRGIVEQCCSICSLYQLENYC 109

Db      |||||||LQPLALEGSLOKRGIVEQCCTCSLYQLENYC 256
Db      82 LEGSLQKRGIVEQCCSICSLYQLENYC 109

; RESULT 9
US-09-815-229-3
; Sequence 3, Application US/09815229
; Patent No. US20020058614A1
; GENERAL INFORMATION:
; APPLICANT: Filvaroff, Ellen H.
; APPLICANT: Okumu, Franklin W.
; TITLE OF INVENTION: USE OF INSULIN FOR THE TREATMENT OF CARTILAGENOUS DISORDERS
; FILE REFERENCE: P1786R1US
; CURRENT APPLICATION NUMBER: US/09/815, 229
; CURRENT FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: US 60/192,103
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 3
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-815-229-3

Query Match          88.3%; Score 454; DB 9; Length 110;
Best Local Similarity 96.6%; Pred. No. 2.3e-42; Indels 0; Gaps 0;
Matches 85; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy      8 SARPVNQHICSHLVEALYLVCGERGFYPTKTRREADPQVQVELGGGAGS1QPLA 67
Db      22 AAFAVNQHLCGSHLVEALYLVCGERGFYPTKTRREADPQVQVELGGGAGS1QPLA 81
Db      68 LEGSLQKRGIVEQCCSICSLYQLENYC 95

Db      |||||||LQPLALEGSLOKRGIVEQCCTCSLYQLENYC 256
Db      82 LEGSLQKRGIVEQCCSICSLYQLENYC 109

; RESULT 10
US-09-804-409A-9
; Sequence 9, Application US/09804409A
; Patent No. US20020155100A1
; GENERAL INFORMATION:
; APPLICANT: KLEFFER, TIMOTHY J.
; APPLICANT: CHEUNG, ANTHONY T.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR REGULATED PROTEIN
; FILE REFERENCE: 029996/027 8721
; CURRENT APPLICATION NUMBER: US/09/804, 409A
; CURRENT FILING DATE: 2001-03-12
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-804-409A-9

Query Match          88.3%; Score 454; DB 9; Length 110;
Best Local Similarity 96.6%; Pred. No. 2.3e-42; Indels 0; Gaps 0;
Matches 85; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy      8 SARPVNQHICSHLVEALYLVCGERGFYPTKTRREADPQVQVELGGGAGS1QPLA 67
Db      68 LEGSLQKRGIVEQCCSICSLYQLENYC 95
Db      82 LEGSLQKRGIVEQCCSICSLYQLENYC 109

; RESULT 11
US-09-969-748C-6
; Sequence 6, Application US/09969748C
; Publication No. US20030161809A1
; GENERAL INFORMATION:
; APPLICANT: ARIZBE PHARMACEUTICALS, INC.
; APPLICANT: HOUSTON, Lou, I.
; APPLICANT: SHERIDAN, Philip, J.
; APPLICANT: HAWLEY, Stephen
; APPLICANT: GLYNN, Jacqueline, M.
; APPLICANT: CHAPIN, Steven
; APPLICANT: BASU, Amresh
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TRANSPORT OF BIOLOGICALLY ACTIVE
; FILE REFERENCE: 057220-0303
; CURRENT APPLICATION NUMBER: US/09/969, 748C
; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: US 60/267, 601
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 60/248, 819
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/248, 478
; PRIOR FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: US 60/237, 929
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-969-748C-6

Query Match          88.3%; Score 454; DB 10; Length 110;
Best Local Similarity 96.6%; Pred. No. 2.3e-42; Indels 0; Gaps 0;
Matches 85; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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RESULT 12
US-09-963-693-125
; Sequence 125, Application US/09963693
; Publication No. US20030181364A1
; GENERAL INFORMATION:
; APPLICANT: Ruvkun, Gary
; APPLICANT: Ogg, Scott
; TITLE OF INVENTION: IMPAIRED GLUCOSE TOLERANCE TOOLS FOR
; PILIE REFERENCE: 00786/351004
; CURRENT APPLICATION NUMBER: US/09/963, 693
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/205, 658
; PRIOR FILING DATE: 1998-12-03
; PRIOR APPLICATION NUMBER: 08/837, 076
; PRIOR FILING DATE: 1997-05-15
; PRIOR APPLICATION NUMBER: 08/888, 534
; PRIOR FILING DATE: 1997-07-07
; PRIOR APPLICATION NUMBER: US8/11080
; PRIOR FILING DATE: 1998-03-15
; NUMBER OF SEQ ID NOS: 328
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 125
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-963-693-125

Query Match 88.3%; Score 454; DB 10; Length 110;
Best Local Similarity 96.6%; Pred. No. 2.3e-42; Indels 0; Gaps 0;
Matches 85; Conservative 1; Mismatches 2; Seq ID NO: 2
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-328-813-2

Query Match 88.3%; Score 454; DB 14; Length 110;
Best Local Similarity 96.6%; Pred. No. 2.3e-42; Indels 0; Gaps 0;
Matches 85; Conservative 1; Mismatches 2; Seq ID NO: 2
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-328-813-2

RESULT 13
US-10-038-686-1
; Sequence 1, Application US/10038686
; Publication No. US20030045467A1
; GENERAL INFORMATION:
; APPLICANT: Orban, Tihamer
; TITLE OF INVENTION: AUTOANTIGEN VACCINE
; FILE REFERENCE: 10276-067001
; CURRENT APPLICATION NUMBER: US/10/038, 686
; CURRENT FILING DATE: 2002-05-31
; PRIOR APPLICATION NUMBER: 6/0/260, 068
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-038-686-1

Query Match 86.3%; Score 454; DB 14; Length 110;
Best Local Similarity 96.6%; Pred. No. 2.3e-42; Indels 0; Gaps 0;
Matches 85; Conservative 1; Mismatches 2; Seq ID NO: 2
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-038-686-1

RESULT 14
US-10-328-813-2
; Sequence 2, Application US/10328813
; Publication No. US20030113305A1
; GENERAL INFORMATION:
; APPLICANT: Osborne, William R. A.
; APPLICANT: Ramash, Nagarajan
; TITLE OF INVENTION: Compositions and Methods for Treating Diabetes
; FILE REFERENCE: P-UW 3264
; CURRENT APPLICATION NUMBER: US/10/328, 813
; CURRENT FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: US/09/185, 852
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: 60/087, 660
; PRIOR FILING DATE: 1998-06-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 2
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-328-813-2

Query Match 88.3%; Score 454; DB 10; Length 110;
Best Local Similarity 96.6%; Pred. No. 2.3e-42; Indels 0; Gaps 0;
Matches 85; Conservative 1; Mismatches 2; Seq ID NO: 2
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-328-813-2

RESULT 15
US-10-346-53-2
; Sequence 2, Application US/10346563
; Publication No. US20030220229A1
; GENERAL INFORMATION:
; APPLICANT: Hickey, William F.
; APPLICANT: Griffin, Ann C.
; TITLE OF INVENTION: Proinsulin Peptide Compounds for Detecting and
; Treating Type I Diabetes
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/346, 563
; FILING DATE: 16-Jan-2003
; PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US/08/472,704
FILING DATE: 06-JUN-1995
APPLICATION NUMBER: US 08/272,220
FILING DATE: 08-JULY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Deconti, Giulio A., Jr.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: DCI-092
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 110 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-346-563-2

Query Match 88.3%; Score 454; DB 15; Length 110;
Best Local Similarity 96.6%; Pred. No. 2; Je-42;
Matches 85; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
CQY 8 SARTVNHQGGSHIVELWLVCGERGFPTPKRREADPQVQVELGGPGAGS1QPLA 67
Db 22 AAARVNQHICGSHIVELWLVCGERGFPTPKRREADLQVQVELGGPGAGS1QPLA 81
QY 68 LEGSLQKRGIVVEOCCTSICSLYOLENYC 95
Db 82 LEGSLQKRGIVVEOCCTSICSLYOLENYC 109

Search completed: May 20, 2005, 00:44:43
Job time : 137 secs

R; Wettemann, W.; Groneberg, J.; Leineweber, M.; Wengenmayer, F.; Winnacker, E.L.
 Gene 19, 175-183, 1982
 A; Title: The nucleotide sequence of cDNA coding for preproinsulin from the primate Macac
 A; Reference number: JQ0178; MUID:83080474; PMID:6184262
 A; Accession: JQ0178
 A; Molecule type: mRNA
 A; Residues: 1-110 <WET>
 A; Cross-references: UNIPROT:P30406; GB:J00336; NID:9342121; PIDN:AAA36849.1; PID:9342122
 C; Superfamily: insulin
 F; 1-24/Domain: signal sequence #status predicted <SIG>
 F; 25-54'/Domain: insulin connecting C-peptide #status predicted <BCH>
 F; 25-54/Domain: insulin chain B #status predicted <BCH>
 F; 55-89/Domain: insulin chain A #status predicted <ACh>
 F; 90-110/Domain: insulin chain A #status predicted <CPEP>
 F; 31-96,43-109,95-100/Disulfide bonds: #status predicted

Query Match 89.5%; Score 460; DB 2; Length 110;
 Best Local Similarity 100.0%; Pred. No. 6.9e-43; Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 11 FVNOHLCGSHLVEALIVCGERGPYPKTRRAEDPQVGQVELGGPGAGSLSLOPLALEG 70
 Db 25 FVNOHLCGSHLVEALIVCGERGPYPKTRRAEDPQVGQVELGGPGAGSLSLOPLALEG 84

Qy 71 SLQRGIVEQCCSICSIKLYOLENYC 95
 Db 85 SLQRGIVEQCCSICSIKLYOLENYC 109

RESULT 3

IPNU insulin precursor [validated] - human
 N; Alternate names: preproinsulin
 C; Species: Homo Sapiens (man)
 C; Date: 23-Oct-1981 #sequence revision 23-Oct-1981 #text change 09-Jul-2004
 C; Accession: A93222; A94253; A93216; A94251; A93144; A92075; A91186; I58114; A01579; S58
 R; Bell, G.I.; Pictet, R.J.; Rutter, W.J.; Cordell, B.; Tischer, E.; Goodman, H.M.;
 Nature 284, 26-32, 1980
 A; Title: Sequence of the human insulin gene.
 A; Reference number: A93222; MUID:80120725; PMID:6243748
 A; Accession: A93222
 A; Molecule type: DNA
 A; Residue: 1-110 <BEL>
 A; Cross-references: UNIPROT:P01308; GB:J00265; NID:918629; PIDN:AAA59179.1; PID:9307072
 R; Bell, G.I.; Pictet, R.; Goodman, H.M.; Rutter, W.J.
 Nature 282, 525-527, 1979
 A; Title: Nucleotide sequence of a cDNA clone encoding human preproinsulin.
 A; Reference number: A93216; MUID:80054779; PMID:503234
 A; Accession: A93216
 A; Molecule type: mRNA
 A; Residues: 1-110 <BEL>
 A; Cross-references: GB:J00265; NID:9186429; PIDN:AAA59172.1; PID:9386828
 R; Surles, I.; Geeddel, D.V.; Gray, A.; Ulrich, A.
 Science 209, 612-615, 1980
 A; Title: Genetic variation in the human insulin gene.
 A; Reference number: A94253; MUID:80236313; PMID:6248962
 A; Accession: A94253
 A; Molecule type: DNA
 A; Residues: 1-110 <ULI>
 A; Cross-references: GB:J00265; NID:9186429; PIDN:AAA59172.1; PID:9386828
 R; Bell, G.I.; Shain, W.F.; Pictet, R.; Cordell, B.; Goodman, H.M.; Rutter, W.J.
 Nature 282, 525-527, 1979
 A; Title: Nucleotide sequence of a cDNA clone encoding human preproinsulin.
 A; Reference number: A93216; MUID:80054779; PMID:503234
 A; Accession: A93216
 A; Molecule type: mRNA
 A; Residues: 1-110 <BEL>
 A; Cross-references: GB:J00265; NID:9186429; PIDN:AAA59172.1; PID:9386828
 R; Surles, I.; Geeddel, D.V.; Gray, A.; Ulrich, A.
 Science 209, 57-59, 1980
 A; Title: Nucleotide sequence of human proproinsulin complementary DNA.
 A; Reference number: A94251; MUID:80147417; PMID:6927840
 A; Accession: A94251
 A; Molecule type: mRNA
 A; Residues: 1-110 <SUR>
 A; Cross-references: GB:J00265; NID:9186429; PIDN:AAA59172.1; PID:9386828
 R; Nicol, D.S.H.W.; Smith, L.F.
 Nature 187, 483-485, 1960
 A; Title: Amino-acid sequence of human insulin.
 A; Reference number: A93144
 A; Accession: A93144

A; Molecule type: protein
 A; Residues: 57-87 <OYE>
 R; Ko, A.; Smyth, D.G.; Markussen, J.; Sundby, F.
 Eur. J. Bioch. 246, 137-1386, 1971
 A; Title: Studies on human proinsulin. Isolation and amino acid sequence of the human pan
 A; Reference number: A92075; MUID:7116410; PMID:5101771
 A; Accession: A92075
 A; Molecule type: protein
 A; Residues: 57-87 <RKA>
 R; Lucasen, A.M.; Beressi, J.P.; Boitard, C.; Frognel, P.; Lathrop, M.; Bell
 Nature Genet. 4, 305-310, 1993
 A; Title: Susceptibility to insulin dependent diabetes mellitus maps to a 4.1 kb segment
 A; Reference number: I58114; MUID:9336428; PMID:8358440
 A; Accession: I58114
 A; Status: preliminary; translated from GB/EMBL/DBJ
 A; Molecule type: DNA
 A; Residues: 1-59,63-110 <RES>
 A; Cross-references: GB:L154470; NID:9307071; PIDN:AAA59179.1; PID:9307072
 R; Sieber, P.; Kamber, B.; Hartmann, A.; Joahl, A.; Riniker, B.; Rittel, W.
 Helv. Chim. Acta 57, 2617-2621, 1974
 A; Title: Totalsynthese von Humaninsulin unter gezielter Bildung der Disulfidbindungen.
 A; Reference number: A91636; MUID:7507777; PMID:4443293
 A; Contents: annotation; synthesis
 A; Note: disulfide-bonded human insulin was synthesized; the synthetic hormone was identi
 A; Note: article in German with English abstract
 R; Naithani, V.K.
 Hoppe-Seyler's Z. Physiol. Chem. 354, 659-672, 1973
 A; Title: The synthesis of C-peptide of human proinsulin.
 A; Reference number: A91558; MUID:7504007; PMID:480504
 A; Contents: annotation; synthesis of residues 57-87
 R; Geiger, R.; Jaeger, G.; Koening, W.
 Chem.-Ber. 106, 2347-2352, 1973
 A; Title: Synthesis of the complete sequence of human proinsulin C-peptide and its [Glu-9
 A; Reference number: A9014
 A; Contents: annotation; synthesis of residues 57-87
 R; Kaufmann, J.E.; Timmerer, J.C.; Halban, P.A.
 Biochem. J. 310, 869-874, 1995
 A; Title: Sequence requirements for proinsulin processing at the B-chain/C-peptide junct
 A; Reference number: S58611; MUID:9501319; PMID:7575420
 A; Content: annotation; site-directed mutagenesis study of proteolytic processing
 C; Genetics:
 A; Gene: GDB:INS
 A; Cross-references: GDB:119349; OMIM:176730
 A; Map Position: 11p15.5-11p15.5
 A; Introns: 63/1
 C; Superfamily: insulin
 C; Keywords: hormone; pancreas
 F; 1-24/Domain: signal sequence #status predicted <SIG>
 F; 25-54/Domain: insulin chain B #status experimental <BCH>
 F; 25-54, 90-110/Product: insulin #status experimental <MAT>
 F; 57-87/Domain: connecting C-peptide #status experimental <CPBP>
 F; 90-110/Domain: insulin chain A #status experimental <ACh>
 F; 31-96,43-109,95-100/Disulfide bonds: #status experimental
 Query Match 88.3%; Score 455; DB 1; Length 110;
 Best Local Similarity 96.6%; Pred. No. 3.1e-42; Matches 85; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 Qy 8 SARFVNQHLCGSHLVEALIVCGERGPYPKTRRAEDPQVGQVELGGPGAGSLSLOPLA 67
 Db 22 AAFAFNQHLCGSHLVEALIVCGERGPYPKTRRAEDPQVGQVELGGPGAGSLSLOPLA 81
 Qy 68 LEGSIIQKRGIVEQCCSICSIKLYOLENYC 95
 Db 82 LEGSIIQKRGIVEQCCSICSIKLYOLENYC 109

RESULT 4

A2179 insulin precursor - chimpanzee

C;Species: Pan troglodytes (chimpanzee)

C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004

C;Accession: A42179; S22058

R;Seino, S.; Bell, G.I.; Li, W.H.

Mol. Biol. Evol. 9, 193-203, 1992

A;Title: Sequences of primate insulin genes support the hypothesis of a slower rate of m

A;Reference number: A42179

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-110 <SEI>

A;Cross-references: UNIPROT:P30410; EMBL:X61089; NID:938251; PIDN:CAA43403.1; PID:938252

A;Note: sequence extracted from NCBI backbone (NCBIP:95067)

C;Genetics:

A;Introns: 63/1

C;Superfamily: insulin

C;Keywords:

INRB

insulin precursor - rabbit

N;Alternate name: preproinsulin

C;Species: Oryctolagus cuniculus (domestic rabbit)

C;Date: 24-Apr-1984 #sequence_revision 23-Aug-1997 #text_change 09-Jul-2004

C;Accession: A53438; A01581

J. Devabhar, S.U.; Giddings, S.J.; Rajakumar, P.A.; Carnaghi, L.R.; Menon, R.K.; Zahm, D.

J. Biol. Chem. 269, 8445-8454, 1994

A;Title: Insulin gene expression and insulin synthesis in mammalian neuronal cells.

A;Reference number: A53438; MUID:94179230; PMID:8132571

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-110 <DEV>

A;Cross-references: UNIPROT:P01311; GB:U03610; NID:9467970; PIDN:AAA19033.1; PID:9467971

R;Smith, L.F.

Am. J. Med. 40, 662-666, 1966

A;Title: Species variation in the amino acid sequence of insulin.

A;Reference number: A9029; MUID:6616019; PMID:594593

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-110 <SMI>

C;Superfamily: insulin

C;Keywords: hormone; pancreas

F;1-24/Domain: signal sequence #status predicted <SIG>

F;25-54/Domain: insulin chain B #status experimental <BCB>

F;25-54, 90-110/Product: insulin #status experimental <MAT>

F;57-87/Domain: connecting peptide #status predicted <CPBP>

F;80-110/Domain: insulin chain A #status experimental <ACH>

F;31-96, 43-109, 95-100/Disulfide bonds: #status experimental

Query Match

Best Local Similarity 78.6%; Score 404; DB 1; Length 110;

Matches 75; Conservative 88.2%; Pred. No. 8; Se-37; 1; Mismatches 9; Indels 0; Gaps 0;

C;Keywords: hormone; pancreas

F;1-24/Domain: insulin chain B #status predicted <BCB>

F;25-54/Domain: insulin chain A #status experimental <ACH>

F;25-54, 90-110/Product: insulin #status experimental <MAT>

F;57-87/Domain: connecting peptide #status predicted <CPBP>

F;90-110/Domain: insulin chain A #status experimental <ACH>

F;31-96, 43-109, 95-100/Disulfide bonds: #status predicted

Query Match

Best Local Similarity 80.0%; Score 411; DB 1; Length 110;

Matches 76; Conservative 89.4%; Pred. No. 1; Se-37; 6; Mismatches 0; Indels 0; Gaps 0;

C;Keywords: hormone; pancreas

F;1-24/Domain: insulin chain B #status experimental <BCB>

F;25-54, 90-110/Product: insulin #status experimental <MAT>

F;57-87/Domain: connecting peptide #status predicted <CPBP>

F;90-110/Domain: insulin chain A #status experimental <ACH>

F;31-96, 43-109, 95-100/Disulfide bonds: #status predicted

Query Match

Best Local Similarity 89.4%; Pred. No. 1; Se-37; 6; Mismatches 0; Indels 0; Gaps 0;

C;Keywords: hormone; pancreas

F;1-24/Domain: insulin chain B #status predicted <BCB>

F;25-54, 90-110/Product: insulin #status experimental <MAT>

F;57-87/Domain: connecting peptide #status predicted <CPBP>

F;90-110/Domain: insulin chain A #status experimental <ACH>

F;31-96, 43-109, 95-100/Disulfide bonds: #status predicted

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Best Local Similarity 89.4%; Pred. No. 1; Se-37; 6; Mismatches 0; Indels 0; Gaps 0;

C;Keywords: hormone; pancreas

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F;25-54, 90-110/Product: insulin #status experimental <MAT>

F;57-87/Domain: connecting peptide #status predicted <CPBP>

F;90-110/Domain: insulin chain A #status experimental <ACH>

F;31-96, 43-109, 95-100/Disulfide bonds: #status predicted

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Best Local Similarity 89.4%; Pred. No. 1; Se-37; 6; Mismatches 0; Indels 0; Gaps 0;

C;Keywords: hormone; pancreas

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F;25-54, 90-110/Product: insulin #status experimental <MAT>

F;57-87/Domain: connecting peptide #status predicted <CPBP>

F;90-110/Domain: insulin chain A #status experimental <ACH>

F;31-96, 43-109, 95-100/Disulfide bonds: #status predicted

Query Match

Best Local Similarity 89.4%; Pred. No. 1; Se-37; 6; Mismatches 0; Indels 0; Gaps 0;

C;Keywords: hormone; pancreas

F;1-24/Domain: insulin chain B #status predicted <BCB>

F;25-54, 90-110/Product: insulin #status experimental <MAT>

F;57-87/Domain: connecting peptide #status predicted <CPBP>

F;90-110/Domain: insulin chain A #status experimental <ACH>

F;31-96, 43-109, 95-100/Disulfide bonds: #status predicted

Query Match

Best Local Similarity 89.4%; Pred. No. 1; Se-37; 6; Mismatches 0; Indels 0; Gaps 0;

C;Keywords: hormone; pancreas

F;1-24/Domain: insulin chain B #status predicted <BCB>

F;25-54, 90-110/Product: insulin #status experimental <MAT>

F;57-87/Domain: connecting peptide #status predicted <CPBP>

F;90-110/Domain: insulin chain A #status experimental <ACH>

F;31-96, 43-109, 95-100/Disulfide bonds: #status predicted

Query Match

Best Local Similarity 89.4%; Pred. No. 1; Se-37; 6; Mismatches 0; Indels 0; Gaps 0;

C;Keywords: hormone; pancreas

F;1-24/Domain: insulin chain B #status predicted <BCB>

F;25-54, 90-110/Product: insulin #status experimental <MAT>

F;57-87/Domain: connecting peptide #status predicted <CPBP>

F;90-110/Domain: insulin chain A #status experimental <ACH>

F;31-96, 43-109, 95-100/Disulfide bonds: #status predicted

Query Match

Best Local Similarity 89.4%; Pred. No. 1; Se-37; 6; Mismatches 0; Indels 0; Gaps 0;

C;Keywords: hormone; pancreas

F;1-24/Domain: insulin chain B #status predicted <BCB>

F;25-54, 90-110/Product: insulin #status experimental <MAT>

F;57-87/Domain: connecting peptide #status predicted <CPBP>

F;90-110/Domain: insulin chain A #status experimental <ACH>

F;31-96, 43-109, 95-100/Disulfide bonds: #status predicted

Query Match

Best Local Similarity 89.4%; Pred. No. 1; Se-37; 6; Mismatches 0; Indels 0; Gaps 0;

C;Keywords: hormone; pancreas

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F;25-54, 90-110/Product: insulin #status experimental <MAT>

F;57-87/Domain: connecting peptide #status predicted <CPBP>

F;90-110/Domain: insulin chain A #status experimental <ACH>

F;31-96, 43-109, 95-100/Disulfide bonds: #status predicted

Query Match

Best Local Similarity 89.4%; Pred. No. 1; Se-37; 6; Mismatches 0; Indels 0; Gaps 0;

C;Keywords: hormone; pancreas

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F;25-54, 90-110/Product: insulin #status experimental <MAT>

F;57-87/Domain: connecting peptide #status predicted <CPBP>

F;90-110/Domain: insulin chain A #status experimental <ACH>

F;31-96, 43-109, 95-100/Disulfide bonds: #status predicted

Query Match

Best Local Similarity 89.4%; Pred. No. 1; Se-37; 6; Mismatches 0; Indels 0; Gaps 0;

C;Keywords: hormone; pancreas

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F;25-54, 90-110/Product: insulin #status experimental <MAT>

F;57-87/Domain: connecting peptide #status predicted <CPBP>

F;90-110/Domain: insulin chain A #status experimental <ACH>

F;31-96, 43-109, 95-100/Disulfide bonds: #status predicted

Query Match

Best Local Similarity 89.4%; Pred. No. 1; Se-37; 6; Mismatches 0; Indels 0; Gaps 0;

C;Keywords: hormone; pancreas

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F;25-54, 90-110/Product: insulin #status experimental <MAT>

F;57-87/Domain: connecting peptide #status predicted <CPBP>

F;90-110/Domain: insulin chain A #status experimental <ACH>

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Query Match

Best Local Similarity 89.4%; Pred. No. 1; Se-37; 6; Mismatches 0; Indels 0; Gaps 0;

C;Keywords: hormone; pancreas

F;1-24/Domain: insulin chain B #status predicted <BCB>

F;25-54, 90-110/Product: insulin #status experimental <MAT>

F;57-87/Domain: connecting peptide #status predicted <CPBP>

F;90-110/Domain: insulin chain A #status experimental <ACH>

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Best Local Similarity 89.4%; Pred. No. 1; Se-37; 6; Mismatches 0; Indels 0; Gaps 0;

C;Keywords: hormone; pancreas

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F;25-54, 90-110/Product: insulin #status experimental <MAT>

F;57-87/Domain: connecting peptide #status predicted <CPBP>

F;90-110/Domain: insulin chain A #status experimental <ACH>

F;31-96, 43-109, 95-100/Disulfide bonds: #status predicted

Query Match

Best Local Similarity 89.4%; Pred. No. 1; Se-37; 6; Mismatches 0; Indels 0; Gaps 0;

C;Keywords: hormone; pancreas

F;1-24/Domain: insulin chain B #status predicted <BCB>

F;25-54, 90-110/Product: insulin #status experimental <MAT>

F;57-87/Domain: connecting peptide #status predicted <CPBP>

F;90-110/Domain: insulin chain A #status experimental <ACH>

F;31-96, 43-109, 95-100/Disulfide bonds: #status predicted

Query Match

Best Local Similarity 89.4%; Pred. No. 1; Se-37; 6; Mismatches 0; Indels 0; Gaps 0;

C;Keywords: hormone; pancreas

F;1-24/Domain: insulin chain B #status predicted <BCB>

F;25-54, 90-110/Product: insulin #status experimental <MAT>

F;57-87/Domain: connecting peptide #status predicted <CPBP>

F;90-110/Domain: insulin chain A #status experimental <ACH>

F;31-96, 43-109, 95-100/Disulfide bonds: #status predicted

Query Match

Best Local Similarity 89.4%; Pred. No. 1; Se-37; 6; Mismatches 0; Indels 0; Gaps 0;

C;Keywords: hormone; pancreas

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F;31-96, 43-109, 95-100/Disulfide bonds: #status predicted

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Best Local Similarity 89.4%; Pred. No. 1; Se-37; 6; Mismatches 0; Indels 0; Gaps 0;

C;Keywords: hormone; pancreas

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F;31-96, 43-109, 95-100/Disulfide bonds: #status predicted

Query Match

Best Local Similarity 89.4%; Pred. No. 1; Se-37; 6; Mismatches 0; Indels 0; Gaps 0;

C;Keywords: hormone; pancreas

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F;25-54, 90-110/Product: insulin #status experimental <MAT>

F;57-87/Domain: connecting peptide #status predicted <CPBP>

F;90-110/Domain: insulin chain A #status experimental <ACH>

F;31-96, 43-109, 95-100/Disulfide bonds: #status predicted

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Best Local Similarity 89.4%; Pred. No. 1; Se-37; 6; Mismatches 0; Indels 0; Gaps 0;

C;Keywords: hormone; pancreas

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F;25-54, 90-110/Product: insulin #status experimental <MAT>

F;57-87/Domain: connecting peptide #status predicted <CPBP>

F;90-110/Domain: insulin chain A #status experimental <ACH>

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Query Match

Best Local Similarity 89.4%; Pred. No. 1; Se-37; 6; Mismatches 0; Indels 0; Gaps 0;

C;Keywords: hormone; pancreas

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F;25-54, 90-110/Product: insulin #status experimental <MAT>

F;57-87/Domain: connecting peptide #status predicted <CPBP>

F;90-110/Domain: insulin chain A #status experimental <ACH>

F;31-96, 43-109, 95-100/Disulfide bonds: #status predicted

Query Match

Best Local Similarity 89.4%; Pred. No. 1; Se-37; 6; Mismatches 0; Indels 0; Gaps 0;

C;Keywords: hormone; pancreas

F;1-24/Domain: insulin chain B #status predicted <BCB>

F;25-54, 90-110/Product: insulin #status experimental <MAT>

F;57-87/Domain: connecting peptide #status predicted <CPBP>

F;90-110/Domain: insulin chain A #status experimental <ACH>

F;31-96, 43-109, 95-100/Disulfide bonds: #status predicted

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Best Local Similarity 89.4%; Pred. No. 1; Se-37; 6; Mismatches 0; Indels 0; Gaps 0;

C;Keywords: hormone; pancreas

F;1-24/Domain: insulin chain B #status predicted <BCB>

F;25-54, 90-110/Product: insulin #status experimental <MAT>

F;57-87/Domain: connecting peptide #status predicted <CPBP>

F;90-110/Domain

A;Reference number: A92120; MUID:73061498; PMID:4640931
A;Accession: A92120
A;Molecule type: protein
A;Residues: 33-63 <TAG>
C;Comment: X's at positions 31-32 and 64-65 represent paired basic residues assumed by C;Superfamily: insulin
C;Keywords: hormone; pancreas
F;1-30//Domain: insulin chain B #status experimental <BCH>
F;1-30, 66-86//Product: insulin #status experimental <MAT>
F;33-63//Domain: connecting peptide #status experimental <CPEP>
F;66-86//Domain: insulin chain A #status experimental <ACH>
F;7-72, 19-85, 71-76//Disulfide bonds: #status predicted

Query Match 77.4%; Score 398; DB 1; Length 86;
Best Local Similarity 85.9%; Pred. No. 3.e-36; 8; Indels 0; Gaps 0;
Matches 73; Conservative 1; Mismatches 4;

Qy 11 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRRAEDPQVQVELGGPGAGSLOPLALEG 70
Db 1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRRAEDPQVQVELGGPGAGSLOPLALEG 60

Qy 71 SLQKRKGIVEQCCCTSCSLYOLENYC 95
Db 61 PQQXKGIVEQCCCTGICSLYOLENYC 85

RESULT 8

INMS2
insulin 2 precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 31-Mar-1992 #sequence revision 14-Jul-1994 #text_change 09-Jul-2004
C;Accession: A63342; B48172; A61012; B01592
R;Westworth, B.M.; Schaefer, I.M.; Villa-Komaroff, L.; Chirgwin, J.M.
J; Mol. Evol. 23, 305-312, 1986
A;Title: Characterization of the two nonallelic genes encoding mouse preproinsulin.
A;Reference number: A92965; MUID:87169768; PMID:3104603
A;Accession: A20342
A;Molecule type: DNA
A;Residues: 1-110 <WYN>
A;Cross-references: UNIPROT:P01326; GB:X04724; NID:952714; PIDN:CRA28433.1; PID:952715
R;Sawa, T.; Ohkura, S.; Morioka, H.; Yano, S.
J; Mol. Endocrinol. 5, 61-67, 1990
A;Title: Molecular cloning and DNA sequence analysis of preproinsulin genes in the NON RT
A;Reference number: A48172; MUID:90372989; PMID:2397023
A;Accession: B48172
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-110 <SW>
R;Linde, S.; Nielsen, J.H.; Hansen, B.; Welinder, B.S.
J; Chromatogr. 462, 243-254, 1989
A;Title: Reversed-phase high-performance liquid chromatographic analyses of insulin biosynthesis
A;Reference number: A61012; MUID:89292078; PMID:2661585
A;Accession: A61012
A;Molecule type: protein
A;Residues: 57-87 <LIIN>
R;Buenzli, H.F.; Glatthaar, B.; Kunz, P.; Muelhaupt, E.; Humbel, R.E.
R;Hoppe-Seyler's Z. Physiol. Chem. 353, 451-458, 1972
A;Title: Amino acid sequence of the two insulins from mouse (Mus musculus).
A;Reference number: A01592; MUID:72189455; PMID:5063718
A;Accession: B01592
A;Molecule type: protein
A;Residues: 25-54;90-110 <BUE>
C;Genetics:
A;Introns: 63/1
C;Superfamily: insulin
C;Keywords: hormone; pancreas
F;1-24//Domain: signal sequence #status predicted <SIG>
F;25-54//Domain: insulin chain B #status experimental <BCH>
F;25-54, 90-110//Product: insulin #status experimental <MAT>
F;57-87//Domain: connecting peptide #status experimental <CPEP>
F;90-110//Domain: insulin chain A #status experimental <ACH>
F;31-96, 43-109, 95-100//Disulfide bonds: #status experimental

Query Match 77.4%; Score 398; DB 1; Length 110;
Best Local Similarity 85.9%; Pred. No. 3.e-36; 8; Indels 0; Gaps 0;
Matches 73; Conservative 4; Mismatches 4;

Qy 11 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRRAEDPQVQVELGGPGAGSLOPLALEG 70
Db 25 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRRAEDPQVQVELGGPGAGSLOPLALEG 84

Qy 71 SLQKRKGIVEQCCCTSCSLYOLENYC 95
Db 85 ARQRKGIVDQCCCTSCSLYOLENYC 109

RESULT 9

IPRT2
insulin 2 precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 23-Oct-1981 #sequence revision 23-oct-1981 #text_change 09-Jul-2004
C;Accession: B90789; B92231; C92220; I64880; A05193; B92120
R;Lomedico, P.; Rosenthal, N.; Efstratiadis, A.; Gilbert, W.; Kolodner, R.; Tizard, R.
Cell 1, 545-558, 1976
A;Title: The structure and evolution of the two nonallelic rat preproinsulin genes.
A;Reference number: A90789; MUID:80045035; PMID:498284
A;Accession: B90789
A;Molecule type: DNA
A;Residues: 1-110 <LOM>
A;Cross-references: UNIPROT:P01323; GB:J00748; NID:9204958; PIDN:AAA41443.1; PID:9204959
R;Steiner, D.F.; Clark, J.L.; Nolan, C.; Rubenstein, A.H.; Margoliash, E.; Aten, B.; Oye
Recent Prog. Horm. Res. 25, 207-202, 1969
A;Title: Proinsulin and the biosynthesis of insulin.
A;Reference number: A94231; MUID:70067613; PMID:4311938
A;Accession: B94231
A;Molecule type: protein
A;Residues: 25-54;90-110 <STE>
R;Tager, H.S.; Steiner, D.F.
J; Biol. Chem. 247, 7935-7940, 1972
A;Title: Primary structures of the proinsulin connecting peptides of the rat and horse.
A;Reference number: A92120; MUID:73061498; PMID:4640931
A;Accession: C922120
A;Molecule type: protein
A;Residues: 57-87 <TAG>
R;Lomedico, P.T.; Rosenthal, N.; Kolodner, R.; Efstratiadis, A.; Gilbert, W.
Ann. N. Y. Acad. Sci. 343, 425-432, 1980
A;Title: The structure of rat preproinsulin genes.
A;Reference number: 151945; MUID:80240379; PMID:6249167
A;Accession: 164880
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-110 <RES>
A;Cross-references: GB:M25585; NID:9204950; PIDN:AAA41440.1; PID:9204952
C;Genetics:
A;Gene: IN52
A;Introns: 63/1
C;Superfamily: insulin
C;Keywords: hormone; pancreas
F;1-24//Domain: signal sequence #status predicted <SIG>
F;25-54//Domain: insulin chain B #status experimental <BCH>
F;25-54, 90-110//Product: insulin #status experimental <MAT>
F;57-87//Domain: connecting peptide #status experimental <CPEP>
F;90-110//Domain: insulin chain A #status experimental <ACH>
F;31-96, 43-109, 95-100//Disulfide bonds: #status experimental

Query Match 77.4%; Score 398; DB 1; Length 110;
Best Local Similarity 85.9%; Pred. No. 3.e-36; 8; Indels 0; Gaps 0;
Matches 73; Conservative 4; Mismatches 4;

Qy 11 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRRAEDPQVQVELGGPGAGSLOPLALEG 70
Db 25 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRRAEDPQVQVELGGPGAGSLOPLALEG 84

Qy 71 SLQKRKGIVEQCCCTSCSLYOLENYC 95
Db 85 ARQRKGIVDQCCCTSCSLYOLENYC 109

RESULT 10
 148156
 insulin precursor - golden hamster
 C;Species: *Mesocricetus auratus* (golden hamster)
 C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 16-Jul-1999
 C;Accession: I18156
 R;Bell, G.I.; Sanchez-Pescador, R.
 A;Title: sequence of a cDNA encoding Syrian hamster preproinsulin.
 A;Reference number: 148156; MUID:84133036; PMID:6365663
 A;Status: preliminary; translated from GB/EMBL/DDJB
 A;Molecule type: mRNA
 A;Residues: 1-110 <RES>
 A;Cross-references: GB:W26328; NID:9191420; PID:AAA37089.1; PID:9305360
 C;Superfamily: Insulin

Query Match 77.0%; Score 396; DB 2; Length 110;
 Best Local Similarity 85.9%; Pred. No. 6.3e-36; F;1-24/Domain: insulin chain B #status experimental <BCH>
 Matches 73; Conservative 4; Mismatches 8; Indels 0; Gaps 0;
 F;25-54/Domain: insulin #status experimental <MAT>
 F;25,54,90-110/Product: insulin #status experimental <CPBP>
 F;57-87/Domain: connecting peptide #status experimental <ACh>
 F;90-110/Domain: insulin chain A #status experimental <ACH>
 F;31-96,43-109,95-100/Disulfide bonds: #status experimental

Query Match 75.7%; Score 389; DB 1; Length 110;
 Best Local Similarity 84.7%; Pred. No. 3.6e-35; F;1-24/Domain: insulin chain B #status experimental <BCH>
 Matches 72; Conservative 4; Mismatches 9; Indels 0; Gaps 0;
 F;25-54/Domain: insulin #status experimental <MAT>
 F;25,54,90-110/Product: insulin #status experimental <CPBP>
 F;57-87/Domain: connecting peptide #status experimental <ACh>
 F;90-110/Domain: insulin chain A #status experimental <ACH>
 F;31-96,43-109,95-100/Disulfide bonds: #status experimental

Query Match 77.0%; Score 396; DB 2; Length 110;
 Best Local Similarity 85.9%; Pred. No. 6.3e-36; F;1-24/Domain: insulin chain B #status experimental <BCH>
 Matches 73; Conservative 4; Mismatches 8; Indels 0; Gaps 0;
 F;25-54/Domain: insulin #status experimental <MAT>
 F;25,54,90-110/Product: insulin #status experimental <CPBP>
 F;57-87/Domain: connecting peptide #status experimental <ACh>
 F;90-110/Domain: insulin chain A #status experimental <ACH>
 F;31-96,43-109,95-100/Disulfide bonds: #status experimental

Query Match 75.7%; Score 389; DB 1; Length 110;
 Best Local Similarity 84.7%; Pred. No. 3.6e-35; F;1-24/Domain: insulin chain B #status experimental <BCH>
 Matches 72; Conservative 4; Mismatches 9; Indels 0; Gaps 0;
 F;25-54/Domain: insulin #status experimental <MAT>
 F;25,54,90-110/Product: insulin #status experimental <CPBP>
 F;57-87/Domain: connecting peptide #status experimental <ACh>
 F;90-110/Domain: insulin chain A #status experimental <ACH>
 F;31-96,43-109,95-100/Disulfide bonds: #status experimental

RESULT 11
 IPR01
 insulin 1 precursor - rat
 C;Species: *Rattus norvegicus* (Norway rat)
 C;Date: 23-Oct-1981 #sequence revision 23-Oct-1981 #text_change 09-Jul-2004
 C;Accession: A90788; A90789; A94231; B22120; 151945; A01589
 R;Cordeil, B.; Bell, G.; Tischer, E.; DeNoto, F.M.; Ulrich, A.; Pictet, R.; Rutter, W.J.
 Cell 18, 533-543, 1979
 A;Title: Isolation and characterization of a cloned rat insulin gene.
 A;Reference number: A90788; MUID:80045034; PMID:498283
 A;Accession: A90788
 A;Molecule type: DNA
 A;Residues: 1-110 <COR>
 A;Cross-references: UNIPROT:P01322; GB:J00747; NID:9204956; PID:AAA41442.1; PID:9204957
 R;Lomedico, P.; Rosenthal, N.; Efstratiadis, A.; Gilbert, W.; Kolodner, R.; Tizard, R.
 Cell 18, 545-558, 1979
 A;Title: The structure and evolution of the two nonallelic rat preproinsulin genes.
 A;Reference number: A90789; MUID:80045035; PMID:498284
 A;Molecule type: DNA
 A;Residues: 1-110 <LOM>
 R;Steiner, D.F.; Clark, J.L.; Nolan, C.; Rubenstein, A.H.; Margoliash, E.; Aten, B.; Oye
 Recent Prog. Horm. Res. 25, 207-282, 1969
 A;Title: Proinsulin and the biosynthesis of insulin.
 A;Reference number: A94231; MUID:70067613; PMID:4311938
 A;Accession: A94231
 A;Molecule type: protein
 A;Residues: 25-54;50-110 <STE>
 R;Roger, H.S.; Steiner, D.F.
 J. Biol. Chem. 247, 7936-7940, 1972
 A;Title: Primary structures of the proinsulin connecting peptides of the rat and horse.
 A;Reference number: A92120; MUID:73061498; PMID:4640931
 A;Accession: B92120
 A;Molecule type: protein
 A;Residues: 33-38,40-62 <SNR>
 A;Note: the authors report the characterization of a connecting peptide variant lacking *r*.
 A;Accession: B6035
 A;Molecule type: protein
 A;Residues: 33-62 <SNR>
 A;Accession: A60835
 A;Molecule type: protein
 A;Residues: 33-38,40-62 <SNR>
 A;Accession: B6035
 A;Molecule type: protein
 A;Residues: 33-62 <SNR>
 R;Blundell, T.; Dodson, G.; Hodgkin, D.; Mercola, D.
 Adv. Protein Chem. 26, 279-402, 1972
 A;Title: Insulin. the structure in the crystal and its reflection in chemistry and biology
 A;Reference number: A00017
 A;Contents: annotation; X-ray crystallography, 1.9 angstroms
 C;Superfamily: insulin
 C;Keywords: hormone; pancreas
 F;1-30/Domain: insulin chain B #status experimental <BCH>

F;1-30, 64-84;Product: insulin #status experimental <MAT>
 F;33-63;Domain: connecting peptide #status experimental <CPEP>
 F;64-84;Domain: insulin chain A #status experimental <ACH>
 F;7-70, 19-83, 69-74;Disulfide bonds: #status experimental

Query Match Best Local Similarity 75.3%; Score 387; DB 1; Length 84;
 Matches 74; Conservative 1; Mismatches 8; Indels 2; Gaps 1;

Oy 11 FVNQHLCSSHVLVEALYLVCGERGFYPTPKTRREADPDQVGQVLELGGGAGSILQPLAEG 70
 Db 1 FVNQHLCSSHVLVEALYLVCGERGFYPTPKTRREADPDQVGQVLELGGGAGSILQPLAEG 70

Oy 71 SIQKRGIVEQCCSICSLYQLENYC 95
 Db 59 PPQRGIVEQCCSICSLYQLENYC 83

RESULT 13

A3983 insulin precursor - douroucouli
 C;Species: Autotus trivirgatus (douroucouli, night monkey, owl monkey)
 C;Date: 27-Nov-1991 #sequence_change 27-Nov-1991 #text_change 09-Jul-2004
 C;Accession: A3983

R;Seino, S.; Steiner, D.F.; Bell, G.I.
 Proc. Natl. Acad. Sci. U.S.A. 84, 7423-7427, 1987

A;Title: Sequence of a New World primate insulin having low biological potency and immunoreactivity
 A;Reference number: A3983; MUID:88041119; PMID:3118367

A;Accession: A3983
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-108 <SET>
 A;Cross-references: UNIPROT:P10604; GB:J02989; NID:9176555; PIDN:AAA35374.1; PID:9176556
 C;Superfamily: insulin

Query Match Best Local Similarity 73.7%; Score 379; DB 2; Length 108;
 Matches 71; Conservative 4; Mismatches 8; Indels 2; Gaps 1;

Oy 11 FVNQHLCSSHVLVEALYLVCGERGFYPTPKTRREADPDQVGQVLELGGGAGSILQPLAEG 70
 Db 25 FVNQHLCSSHVLVEALYLVCGERGFYPTPKTRREADPDQVGQVLELGGGAGSILQPLAEG 70

Oy 71 SIQKRGIVEQCCSICSLYQLENYC 95
 Db 83 PPQRGIVEQCCSICSLYQLENYC 107

RESULT 14

IPBO insulin precursor - bovine
 C;Species: Bos primigenius taurus (cattle)
 C;Date: 24-Apr-1994 #sequence_revision 22-Apr-1995 #text_change 09-Jul-2004
 C;Accession: A40909; A92000; A92074; A91185; A90342; A90341; S48184; S48185; S46258; A01
 R;D'Agostino, J.; Younes, M.A.; White, J.W.; Besch, P.K.; Field, J.B.; Frazier, M.L.
 Mol. Endocrinol. 1, 327-331, 1987
 A;Title: Cloning and nucleotide sequence analysis of complementary deoxyribonucleic acid
 A;Reference number: A40909; MUID:88288209; PMID:2456452
 A;Accession: A40909
 A;Molecule type: mRNA
 A;Residues: 1-105 <DNA>
 A;Cross-references: UNIPROT:P03171; GB:M54979; NID:9163578; PIDN:AAA30722.1; PID:9163579
 A;Experimental source: fetal pancreas
 R;Nolan, C.; Margolash, E.; Peterson, J.D.; Steiner, D.F.
 J. Biol. Chem. 246, 2780-2795, 1971
 A;Title: The structure of bovine proinsulin.
 A;Reference number: A92080; MUID:7116642; PMID:4928892
 A;Accession: A92080
 A;Molecule type: protein
 A;Residues: 25-105 <NOL>
 A;Cross-references: 25-105 <NOL>
 R;Steiner, D.F.; Cho, S.; Oyer, P.E.; Terris, S.; Peterson, J.D.; Rubenstein, A.H.
 J. Biol. Chem. 246, 1365-1374, 1971
 A;Title: Isolation and characterization of proinsulin C-peptide from bovine pancreas.

Query Match Best Local Similarity 72.1%; Score 370.5; DB 1; Length 105;
 Matches 69; Conservative 2; Mismatches 9; Indels 5; Gaps 1;

Oy 11 FVNQHLCSSHVLVEALYLVCGERGFYPTPKTRREADPDQVGQVLELGGGAGSILQPLAEG 70
 Db 25 FVNQHLCSSHVLVEALYLVCGERGFYPTPKTRREADPDQVGQVLELGGGAGSILQPLAEG 70

Oy 71 SIQKRGIVEQCCSICSLYQLENYC 95
 Db 80 PPQRGIVEQCCSICSLYQLENYC 104

RESULT 15

NMSI

insulin 1 precursor - mouse
 C;Species: Mus musculus (house mouse)
 C;Date: 24-Apr-1984 #sequence_revision 14-Jul-1994 #text_change 09-Jul-2004
 C;Accession: B26342; A48172; A01592; B61012
 R;Mentworth, B.M.; Schaefer, I.M.; Villa-Komaroff, L.; Chirgwin, J.M.
 J. Mol. Biol. 23, 305-312, 1986
 A;Title: Characterization of the two nonallelic genes encoding mouse preproinsulin.
 A;Reference number: A923665; MUID:87169768; PMID:3104603
 A;Accession: B26342
 A;Molecule type: DNA
 A;Residues: 1-108 <WEN>
 A;Cross-references: UNIPROT:R01325; GB:X04725; NID:952712; PIDN:CAA28434.1; PID:952713
 R;Sawa, T.; Oigaku, S.; Morioka, H.; Yano, S.
 J. Mol. Endocrinol. 5, 61-67, 1990
 A;Title: Molecular cloning and DNA sequence analysis of preproinsulin genes in the NON rat
 A;Reference number: A48172; MUID:90372989; PMID:2397023
 A;Accession: A48172
 A;Status: not compared with conceptual translation
 A;Molecule type: DNA
 A;Residues: 1-108 <SAW>
 R;Buenzli, H.P.; Glatthaar, B.; Kunz, P.; Muelhaupt, B.; Humbel, R.E.
 Hoppe-Seyler's Z. Physiol. Chem. 353, 451-458, 1972
 A;Title: Amino acid sequence of the two insulins from mouse (Mus musculus).
 A;Reference number: A01592; MUID:72189455; PMID:5063718
 A;Accession: A01592
 A;Molecule type: protein
 A;Residues: 25-54,88-108 <BU8>
 R;Junde, S.; Nielsen, J.H.; Hansen, B.; Weilander, B.S.
 J. Chromatogr. 462, 243-254, 1989
 A;Title: Reversed-phase high-performance liquid chromatographic analyses of insulin bioactive peptides.
 A;Reference number: A61012; MUID:89292078; PMID:2661585
 A;Molecule type: protein
 A;Residues: 57-85 <LIIN>
 C;Superfamily: insulin
 C;Keywords: hormone; pancreas
 P;1-24/Domain: signal Sequence #status predicted <SIG>
 P;25-54/Domain: insulin chain B #status experimental <BCH>
 P;54-88/Domain: insulin #status experimental <MAT>
 P;88-108/Domain: connecting peptide #status experimental <CPEP>
 P;31-94,43-107,93-98/Disulfide bonds: #status predicted
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 Best local similarity 82.4%; Pred No. 4.2e-33; 9; Indels 2; Gaps 1;
 Matches 70; Conservative 4; Mismatches 9;
 Qy 11 FVNQHLGCGSLVLEAIVLYVGGERGYTPKTRAREDPDQVQELGGPONGSIQPLAEG 70
 Db 25 FVKQHICGPHILVEAIVLYVGGERGYTPKSRREVDPQVQELGGSP--GDLQTLALEV 82
 Qy 71 SLQKRGIVVEQCTSTCSLVLQLENYC 95
 Db 83 ARQERGIVDQCTSCSLVLQLENYC 107
 Search completed: May 20, 2005, 00:42:22
 Job time : 39 sec

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Scoring table:				BLOSUM62									
Gapop 10.0 , Gapext: 0.5													
Searched:				1612378 seqs, 512079187 residues									
Total number of hits satisfying chosen parameters:				1612378									
Minimum DB seq length: 0				DT									
Maximum DB seq length: 200000000				DT									
Post-processing:				0%									
Maximum Match				DE									
Listing first 45 summaries				GN									
Database :				OS									
UniProt: 03:*				OC									
1: uniprot_sprot:*				OC									
2: uniprot_trembl:*				OC									
Pred. No.				is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.									
Result No.				SUMMARIES									
Query Match Length DB ID				Description									
1	460	89.5	110	1	INS_CERAE	P30407	cercopithec	RESULT 1					
2	460	89.5	110	1	INS_MACRAE	P30406	macaca fasc	ID_	INS_CERAE	STANDARD;	PRT;	110 AA.	
3	454	88.3	110	1	INS_GORGO	Q5YK33	gorilla gor	ID_	INS_CERAE	STANDARD;	PRT;	110 AA.	
4	454	88.3	110	1	INS_HUMAN	P01308	homo sapien	AC	P30407; P01309;	STANDARD;	PRT;	110 AA.	
5	451	87.7	110	1	INS_PANTHERA	P30410	pan troglod	DT	01-APR-1993	(Rel.: 25, Created)			
6	450	87.7	110	1	INS_PONPY	P0bxv2	pongo pygma	DT	01-APR-1993	(Rel.: 25, Last sequence update)			
7	411	80.0	110	1	INS_RABBIT	P01311	oryctolagus cuniculus	DT	05-JUL-2004	(Rel.: 44, Last annotation update)			
8	408	79.4	110	1	INS_SIBETR	Q9ixJ3	spermophilus	DE	In insulin precursor				
9	404	78.6	110	1	INS_CANFIA	P01310	canis familiaris	GN	Name=INS;				
10	398	77.4	86	1	INS_HORSE	P01326	equus caballus	OS	Cercopithecus aethiops (Green monkey) (Grivet).				
11	398	77.4	110	1	INS2_MOUSE	P01326	mus musculus	OC	Makazza; Chordata; Craniata; Vertebrata; Euteleostomi;				
12	398	77.4	110	1	INS2_RAT	P01323	rattus norvegicus	OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;				
13	396	77.0	110	1	INS_CIRILO	P01313	cricetulus cricetus	OC	Cercopithecinae; Cercopithecidae.				
14	389	75.7	110	1	INS1_RAT	P01322	rattus norvegicus	RN	NCBI_TaxID=9534;				
15	387	75.3	108	1	INS_PIG	P01315	sus scrofa	RP	SEQUENCE FROM N.A.				
16	381	74.1	110	1	INS_PSKOB	Q62887	peammonys osta	RP	SEQUENCE OF 57-87.				
17	379	73.7	108	1	INS_ACOTR	P06972	actius trivirgatus	RX	MEDLINE=72258016; PubMed=1560757;				
18	375	73.0	110	2	Q8WNW6	J_Biol_Chem.	247:4865-4871(1972).	RA	Steino S., Bell G.I., Li W.;				
19	370.5	72.1	105	1	INS_BOVIN	P01317	bos taurus	RA	"Sequences of primate insulin genes support the hypothesis of a slower rate of molecular evolution in humans and apes than in monkeys.";				
20	370	72.0	108	1	INS1_MOUSE	P01325	mus musculus	RT	Determination of the amino acid sequence of the monkey, sheep, and dog proinsulin C-peptides by a semi-micro Edman degradation procedure";				
21	366.5	71.3	105	1	INS_SRBER	P01318	ovis aries	RT	R. J. Peterson, J.D., Neirlich S., Oyer P.E., Steiner D.F.;				
22	338.5	65.9	108	1	INS_RODSP	P21563	rodentia sp	RT	"Determinant of the amino acid sequence of the monkey, sheep, and dog proinsulin C-peptides by a semi-micro Edman degradation procedure";				
23	335	65.2	65	2	Q8HZ80	P017715	pongo pygmaeus	CC	Q. - FUNCTION: Insulin decreases blood glucose concentration. It increases cell permeability to monosaccharides, amino acids and fatty acids. It accelerates glycogenesis in liver, the pentose phosphate cycle, and glycogen synthesis in liver.				
24	335	65.2	65	2	Q8HZ81	P01323	rattus norvegicus	CC	" - SUBUNIT: Heterodimer of a B chain and an A chain linked by two disulfide bonds.				
25	320	62.3	110	1	INS_CAVPO	P01329	cavia porcellus	CC	-- SIMILARITY: Belongs to the insulin family.				
26	287.5	53.9	103	1	INS_SELRP	P54463	selaspis horvathi	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.ebi-sib.ch/announce/ or send an email to license@ebi-sib.ch).				
27	274.5	53.4	107	1	INS_CHICK	P67970	gallus gallus	CC	EMBL: X61092; CAA34051.1; PIR: B42179; B42179.				
28	271.5	52.8	106	1	INS2_XENLA	P01318	xenopus laevis	CC	HSSP; P01308; IAT10.				
29	268.5	52.2	106	1	INS1_XENLA	P1207	xenopus laevis	CC	InterPro: IPR00425; InsPfam: IPR00449; Insulin: 1.				
30	265	51.6	109	1	INS_OCTOPU	P17715	octodon degus	CC	PRINTS; PR00277; INSULINB.				
31	259.5	50.5	81	1	INS_ANAPL	P01333	anas platyrhynchos	CC	PRODOM: PD05667; Mollusc: ins: 1. SMART: SM00078; Igf: 1.				

RESULT 4

INS_HUMAN	STANDARD;	PRT;	110 AA.
ID INS_HUMAN			
AC P01308;	(Rel. 01, Created)		
DT 21-JUL-1986	(Rel. 01, Last sequence update)		
DT 25-OCT-2004	(Rel. 45, Last annotation update)		
DR Insulin precursor.			
GN Name=INS;			
OS Homo sapiens (Human)			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;			
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX NCBI_TAXID=9606;			
[1] —			
RP SEQUENCE FROM N.A.			
RX MEDLINE-B012025; PubMed=6243748;			
RA Bell G.T., Pictet R.L., Rutter W.J., Cordell B., Tischer E.,			
RA Goodman H.M.,			
RT "Sequence of the human insulin gene.";			
RT Nature 284:26-32(1980).			
RN [2]			
RP SEQUENCE FROM N.A.			
RX MEDLINE-B012313; PubMed=6248962;			
RA Ulrich A., Dull T.J., Gray A., Brosius J., Sures I.,			
RA Rutter W.J.,			
RT "Genetic variation in the human insulin gene.";			
RL Science 209:612-615(1980).			
RN [3]			
RP SEQUENCE FROM N.A.			
RX MEDLINE-B0105479; PubMed=503234;			
RA Bell G.T., Srain W.F., Pictet R.L., Cordell B., Goodman H.M.,			
RA Rutter W.J.,			
RT "Nucleotide sequence of a cDNA clone encoding human preproinsulin.";			
RL Nature 282:525-527(1979).			
RN [4]			
RP SEQUENCE FROM N.A.			
RX MEDLINE-B011471; PubMed=6927840;			
RA Sures I., Goeddel D.V., Gray A., Ulrich A.,			
RT "Nucleotide sequence of human proproinsulin complementary DNA.";			
RL Science 208:57-59(1980).			
RN [5]			
RP SEQUENCE FROM N.A.			
RX MEDLINE-B0136428; PubMed=8358440;			
RA Lucasen A.M., Bell J.T., Julian C., Lathrop M.,			
RT "Susceptibility to insulin dependent diabetes mellitus maps to a 4.1 kb segment of DNA spanning the insulin gene and associated VNTR.";			
RL Nat. Genet. 4:305-310(1993).			
RN [6]			
RP SEQUENCE FROM N.A.			
RC TISSUE=pancreas;			
RX MEDLINE-B22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA Klaunser R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,			
RA Attaschuk S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Blatt N.K.,			
RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA Dratchenko L., Marusina K., Farmer A.X., Rubin G.M., Hong L.,			
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RX			
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,			
RA DISULFID 43 109 Interchain (By similarity).			
PT DISULFID 95 100 By similarity.			
FT DISULFID 110 AA; 11981 MW; C2C3B23B85E52085 CRC64;			
SQ SEQUENCE			
Query Match Best local similarity 88.3%; Score 454; DB 1; Length 110;			
Matches 85; Conservative 1; Mismatches 2; Indels 0; Gaps 0;			
Match 96.6%; Fred. No. 9.3e-39;			
QY 8 SARFYQHQHLCGSHLVEALYLVCGERGFYPPKTRREAPDQGOVLEGGPAGSGLQPLA 67			
Db 22 AAQFVQHQHLCGSHLVEALYLVCGERGFYPPKTRREAPDQGOVLEGGPAGSGLQPLA 81			
QY 69 LEGSLSQKRGIVEQCTSCISLYQLENYC 95			
Db 82 LEGSLSQKRGIVEQCTSCISLYQLENYC 109			

RESULTS

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butterfield Y.S.N., Kozlowski M.I., Skalska U., Smailus D.E.,

RA Schnierch A., Schein J.E., Jones S.J.M., Marra M.A.,

RA and mouse cDNA sequences.";

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

[7]

RP SEQUENCE OF 1-59 FROM N.A.

RC TISSUE=Blood;

RA Falardy I.I., Weill J.J., Stuckens C.C., Danze P.M.P.;

RT "Description of a novel RFLP diallelic polymorphism (-127 BsgI C/G) within the 5' region of insulin gene";

RT Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.

RN [8]

RP SEQUENCE OF 25-54 AND 90-110.

RX PubMed=1426955;

RA Nicol D.S.H.W., Smith L.F.;

RT "Amino-acid sequence of human insulin.";

RN [9]

RP SEQUENCE OF 57-87.

RX MEDLINE-B1116410; PubMed=5101771;

RA Oyer P.E., Cho S., Peterson J.D., Steiner D.F.;

RT "Studies on human proinsulin. Isolation and amino acid sequence of the human pancreatic C-peptide";

RA RL J. Biol. Chem. 246:1375-1386(1971).

RN [10]

RP SEQUENCE OF 57-87.

RX MEDLINE-B1237722; PubMed=5560404;

RA Ko A., Smyth D.G., Marrusen J., Sundby F.;

RT "The amino acid sequence of the C-peptide of human proinsulin.";

RA RL Eur. J. Biochem. 20:190-199(1971).

RN [11]

RP SYNTHESIS.

RX MEDLINE-B7507727; PubMed=4443293;

RA Sieber P., Kamber B., Hartmann A., Joehl A., Riniker B., Rittel W.;

RT "Total synthesis of human insulin under directed formation of the disulfide bonds.";

RA RL Helv. Chim. Acta 57:2617-2621(1974).

RN [12]

RP SYNTHESIS OF 57-87.

RX MEDLINE-B1504007; PubMed=4803504;

RA Naithani V.K.;

RT "Studies on Polypeptides, IV. The synthesis of C-peptide of human proinsulin.";

RT Hoppe-Seyler's Z. Physiol. Chem. 354:659-672(1973).

RN [13]

RP SYNTHESIS OF 65-69 AND 70-73.

RX MEDLINE-B73161263; PubMed=4698555;

RA Geiger R., Volk A.;

RT "Synthesis of peptides with the properties of human proinsulin C peptide (hc peptide). 3. Synthesis of the sequences 14-17 and 9-13 of human proinsulin C peptide.";

RT Chem. Ber. 106:199-205(1973).

RN [14]

RP SYNTHESIS OF 84-87.

RX MEDLINE-B73161261; PubMed=4698553;

RA Geiger R., Jaeger G., Keonig W., Treuth G.;

RT "Synthesis of peptides with the properties of human proinsulin C peptide (hc peptide). I. Scheme for the synthesis and preparation of the sequence 28-31 of human proinsulin C peptide.";

RT Chem. Ber. 106:188-192(1973).

RN [15]

RP VARIANT LOS ANGELES SER-48.

RX MEDLINE-B84016053; PubMed=6312455;

Query Match		Matched Sequence	
		Best Local Similarity	Score
RN	"Studies on mutant human insulin genes: identification and sequence analysis of a gene encoding [SerB2A]insulin;"	96.6%	88.3%; Score 454;
RT	"Studies on mutant human insulin genes: identification and sequence analysis of a gene encoding [SerB2A]insulin;"	96.6%	DB 1; Length 110;
RL	Proc. Natl. Acad. Sci. U.S.A. 80:6366-6370(1983).	1;	Mismatches 2;
RN	[16]	85;	Indels 0;
RP	VARIANT LOS ANGELES SBR-48 AND CHICAGO LEU-49.	Conservative	Gaps 0;
RA	Shoelson S., Flickova M., Hanned M., Nahum A., Musso G., Kaiser E.T., Rubenstein A.H., Tager H.;		
RT	"Identification of a mutant human insulin predicted to contain a serine-for-phenylalanine substitution."		
RT	Proc. Natl. Acad. Sci. U.S.A. 80:7390-7394(1983).		
RN	[17]		
RP	VARIANT PROVIDENCE ASP-34.		
RX	MEDLINE:87115640; PubMed=3470784;		
RA	Chan S.J., Seino S., Gruppuso P.A., Schwartz R., Steiner D.F.;		
RT	"A mutation in the B chain coding region is associated with impaired proinsulin conversion in a family with hyperproinsulinemia;"		
RT	Proc. Natl. Acad. Sci. U.S.A. 84:2194-2197(1987).		
RN	[18]		
RP	VARIANT WAKAYAMA LRU-92.		
RX	MEDLINE:87050122; PubMed=3537011;		
RA	Sakurai H., Iwamoto Y., Sakamoto Y., Kuzuya T., Hirata H.;		
RT	"Structurally abnormal insulin in a diabetic patient. Characterization of the mutant insulin A3 (Val->Ileu) isolated from the pancreas;"		
RL	J. Clin. Invest. 78:1666-1672(1986).		
RN	[19]		
RP	VARIANT HIS-89.		
RX	MEDLINE:90317021; PubMed=2196279;		
RA	Bartelti F., Raben N., Kadowaki T., Cama A., Accili D., Gabay K.H., Merenich J.A., Taylor S.I., Roth J.;		
RT	"Two unrelated patients with familial hyperproinsulinemia due to a mutation substituting histidine for arginine at position 65 in the proinsulin molecule: identification of the mutation by direct sequencing of genomic deoxyribonucleic acid amplified by polymerase chain reaction."		
RL	J. Clin. Endocrinol. Metab. 71:164-169(1990).		
RN	[20]		
RP	VARIANT HIS-89.		
RX	MEDLINE:85261996; PubMed=4019786;		
RA	Shibasaki Y., Kawakami T., Kanazawa Y., Takaku F.;		
RT	"Post-translational cleavage of proinsulin is blocked by a point mutation in familial hyperproinsulinemia;"		
RT	"Two unrelated patients with familial hyperproinsulinemia due to a mutation substituting histidine for arginine at position 65 in the proinsulin molecule: identification of the mutation by direct sequencing of genomic deoxyribonucleic acid amplified by polymerase chain reaction."		
RL	J. Clin. Invest. 76:378-380(1985).		
RN	[21]		
RP	VARIANT KYOTO LEU-89.		
RX	MEDLINE:92291307; PubMed=1601997;		
RA	Yano H., Kitano N., Morimoto M., Polonsky K.S., Imura H., Seino Y.;		
RT	"A novel point mutation in the human insulin gene giving rise to hyperproinsulinemia (proinsulin Kyoto)." ;		
RT	J. Clin. Invest. 89:1902-1907(1992).		
RN	[22]		
RP	STRUCTURE BY NMR.		
RX	MEDLINE:91104966; PubMed=2271664;		
RA	Hua Q.-X., Weiss M.A.;		
RT	"Toward the solution structure of human insulin: sequential 2D 1H NMR assignment of a des-pentapeptide analogue and comparison with crystal structure.";		
RT	Biochemistry 30:5505-5515(1991).		
RL	[23]		
RN	STRUCTURE BY NMR.		
RX	MEDLINE:91242467; PubMed=2036420;		
RA	Hua Q.-X., Weiss M.A.;		
RT	"Comparative 2D NMR studies of human insulin and des-pentapeptide insulin: sequential resonance assignment and implications for protein dynamics and receptor recognition;"		
RT	Biochemistry 30:5505-5515(1991).		
RL	[24]		
RP	STRUCTURE BY NMR.		
RX	MEDLINE:91265527; PubMed=1646635; DOI=10.1016/0167-4838(91)90098-K;		
RA	Hua Q.-X., Weiss M.A.;		
RT	"Two-dimensional NMR studies of Des-(B26-B3)-insulin: sequence-specific resonance assignments and effects of solvent composition;"		
RT			
RP			
RESULT 5			
INS_PANTR	INS_PANTR	STANDARD	PRT; 110 AA.
ID	INS_PANTR		
AC	P30410;		
DT	01-APR-1993 (Rel. 25, Created)		
RT	01-APR-1993 (Rel. 25, Last sequence update)		
DT	25-OCT-2004 (Rel. 45, Last annotation update)		
DE	Insulin precursor.		
OS	Name=INS;		
GN	Pan troglodytes (Chimpanzee);		
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalii; Eutheria; Primates; Catarrhini; Hominidae; Pan.		
OX	NCBI_TaxID=9598;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE:92219953; PubMed=1560757;		
RA	Seino S., Bell G.I., Li W.;		
RT	"Sequences of primate insulin genes support the hypothesis of a slower rate of molecular evolution in humans and apes than in monkey.";		
RL	Mol. Biol. Evol. 9:193-203(1992).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE:2283521; PubMed=12952878; DOI=10.1101/gr.948003;		
RA	Steed J.D.H., Hurles M.E., Jeffreys A.J.;		
RT	"Global haplotype diversity in the human insulin gene region.";		
RL	Genome Res. 13:2101-2111(2003).		
CC	-1- FUNCTION: Insulin decreases blood glucose concentration. It increases cell permeability to monosaccharides, amino acids and fatty acids. It accelerates glycolysis, the pentose phosphate cycle, and glycosylation synthesis in liver.		
CC	-1- SUBUNIT: Heterodimer of a B chain and an A chain linked by two disulfide bonds.		
CC	-1- SUBCELLULAR LOCATION: Secreted.		
CC	-1- SIMILARITY: Belongs to the insulin family.		
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).		
CC	or send an email to license@isb-sib.ch).		
DR	InterPro; IPRO04825; Ins/IGF/relax.		
DR	EMBL; X61089; CAA3403_1; -.		
DR	PFam; PF00049; Insulin; 1.		
DR	PRINTS; PR00277; INSULINB.		
DR	ProDom; P001667; Molusc_ins; 1.		
DR	EMBL; AY137491; AAN06933_1; -.		
DR	PIR; A42179; A42179.		
DR	HSSP; P01308; IAI0.		
DR	InterPro; IPRO04825; Ins/IGF/relax.		
DR	EMBL; X61089; CAA3403_1; -.		
DR	PFam; PF00049; Insulin; 1.		
DR	PRINTS; PR00277; INSULINB.		
DR	ProDom; P001667; Molusc_ins; 1.		
DR	EMBL; AY137491; AAN06933_1; -.		
FT	KW Glucose metabolism; Hormone; insulin family; Signal.		
FT	SIGNAL 1 24 BY Similarity.		
FT	CHAIN 25 54 Insulin B chain.		
FT	PROBP 57 87 C peptide.		
FT	CHAIN 90 110 Insulin A chain.		
FT	DISULFID 31 96 Interchain (By similarity).		
FT	DISULFID 43 109 Interchain (By similarity).		

FT DISULFID 95 100 By similarity.
 SQ SEQUENCE 110 AA; 12025 MW; 41EB8DF79B37CEFS CRC64;
 Query Match 87.7%; Score 45%; DB 1; Length 110;
 Best Local Similarity 95.5%; Fred. No. 1.9e-38;
 Matches 84; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 8 SPARFNQHICCGSHLVEALYLYVCGERGPFYTPKTRREAEDPOVQVELGGGGAGSLOPLA 67
 DB 22 ASAFINQHLOGSHLVEALYLYVCGERGPFYTPKTRREAEDQVQVELGGGGAGSLOPLA 81
 QY 68 LEGSLOQKRGIVEQCCSICSYQLENYC 95
 DB 82 LEGSLOQKRGIVEQCCSICSYQLENYC 109
RESULT 6
 INS_PONPY
 ID INS_PONPY STANDARD; PRT; 110 AA.
 AC Q8HxV2;
 DT 05-JUL-2004 (Rel. 44, last sequence update)
 DT 05-JUL-2004 (Rel. 44, last annotation update)
 DB Insulin precursor.
 Name=INS;
 OS Pongo pygmaeus (Orangutan).
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
 OX NCBI_TAXID=9600;
 RN 11
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22833521; PubMed=12052878; DOI=10.1101/gr.948003;
 RA Stead J.D.H.; Hurles M.E.; Jeffreys A.J.;
 RT "Global haplotype diversity in the human insulin gene region.";
 RL Genome Res. 13:2101-2111(2003).
 CC -- FUNCTION: Insulin decreases blood glucose concentration. It increases cell permeability to monosaccharides, amino acids and fatty acids. It accelerates glycolysis, the pentose phosphate cycle, and glycogen synthesis in liver.
 CC -- SUBUNIT: Heterodimer of a B chain and an A chain linked by two disulfide bonds.
 CC -- SUBCELLULAR LOCATION: Secreted.
 CC -- SIMILARITY: Belongs to the insulin family.
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 CC DR EMBL; AY137503; AACN6937.1; -.
 CC DR PROTEIN; IPRO0425; Ins/IGF-relax.
 CC DR PRINTS; PR00277; INSULINB.
 CC DR PRODOM; PD015667; Mollusc_ins; 1.
 CC DR SMART; SMD0078; IIGF; 1.
 CC DR PROSITE; PS00262; INSULIN; 1.
 KW Glucose metabolism; Hormone; Insulin family; Signal.
 PT SIGNAL 1 24 By similarity.
 PT CHAIN 25 54 Insulin B chain.
 PT PROPEP 57 87 C peptide.
 PT CHAIN 90 110 Insulin A chain.
 PT DISULFID 31 96 Interchain (By similarity).
 PT DISULFID 43 109 Interchain (By similarity).
 PT DISULFID 95 100 By similarity.
 SEQUENCE 110 AA; 12038 MW; 22D2B32B94F520F8 CRC64;
 Query Match 87.5%; Score 450; DB 1; Length 110;
 Best Local Similarity 98.8%; Fred. No. 2.4e-38;
 Matches 84; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 FVNQHLCSSHLLVEALYLYVCGERGPFYTPKTRREAEDPOVQVELGGGGAGSLOPLAEG 70
 DB 25 FVNQHLCSSHLLVEALYLYVCGERGPFYTPKTRREAEDQVQVELGGGGAGSLOPLAEG 84
 QY 71 SLQRGIVEQCCSICSYQLENYC 95
 DB 85 SLQRGIVEQCCSICSYQLENYC 109
RESULT 7
 INS_RABIT
 ID INS_RABIT STANDARD; PRT; 110 AA.
 AC P01311;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-FEB-1996 (Rel. 33, last sequence update)
 DT 05-JUL-2004 (Rel. 44, last annotation update)
 DB Insulin precursor.
 Name=INS;
 OS Oryctolagus cuniculus (Rabbit).
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TAXID=9866; [1]
 RN 11
 RP SEQUENCE FROM N.A.
 RC STRAIN>New Zealand white; TISSUE=Pancreas;
 MEDLINE=94179230; PubMed=8132571;
 RA Devaskar S.U., Giddings S.J., Rajakumar P.A., Carnaghi L.R.,
 RA Menon R.K., Zahm D.S.;
 RT "Insulin gene expression and insulin synthesis in mammalian neuronal cells." J. Biol. Chem. 269:8445-8454(1994).
 RL [2]
 RP SEQUENCE OF 25-54 AND 90-110.
 RX MEDLINE=66160119; PubMed=5949593; DOI=10.1016/0002-9343(66)90145-8;
 RA Smith L.P.; Carnaghi L.R.; Devaskar S.U.;
 RA Gladings S.J.; Carnaghi L.R.; Devaskar S.U.;
 RL Submitted (PAR-1991) to the EMBL/GenBank/DDBJ databases.
 CC -- FUNCTION: Insulin decreases blood glucose concentration. It increases cell permeability to monosaccharides, amino acids and fatty acids. It accelerates glycolysis, the pentose phosphate cycle, and glycogen synthesis in liver.
 CC -- SUBUNIT: Heterodimer of a B chain and an A chain linked by two disulfide bonds.
 CC -- SUBCELLULAR LOCATION: Secreted.
 CC -- SIMILARITY: Belongs to the insulin family.
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 CC DR EMBL; U03610; AAC19033.1; -.
 DR PRODOM; PD015667; Mollusc_ins; 1.
 DR SMART; SMD0078; IIGF; 1.
 DR PROSITE; PS00262; INSULIN; 1.
 KW Direct protein sequencing; Glucose metabolism; Hormone; Insulin family; Signal.
 PT CHAIN 1 24 Insulin B chain.

FT PROPEP 57 87 C peptide.
 FT CHAIN 90 110 Insulin A chain.
 FT DISULFID 31 96 Interchain.
 FT DISULFID 43 109 Interchain.
 FT DISULFID 95 100
 FT CONFLICT 83 E -> Y (in Ref. 3).
 SQ SEQUENCE 110 AA; 11838 MW; 82D2375B85D77FA8 CRC64;
 Query Match 80.0%; Score 411; DB 1; Length 110;
 Best Local Similarity 89.4%; Pred. No. 4.8e-34;
 Matches 76; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
 QY 11 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDPQVQVLEGGPGASSLQPLALEG 70
 25 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDPQVQVLEGGPGASSLQPLALEM 84
 Db 71 SLOKRGIIVEQQCTSTICSLYQLENYC 95
 QY 71 SLOKRGIIVEQQCTSTICSLYQLENYC 95
 85 ALQKRGIVEQCCTSTICSLYQLENYC 109
 Db 85 ALQKRGIVEQCCTSTICSLYQLENYC 109

RESULT 8

INS_SPTR STANDARD; PRT; 110 AA.

ID INS_SPTR 091X13; 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Insulin precursor.
 GN Name=INS; Spermophilus tridecemlineatus (Thirteen-lined ground squirrel).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
 OC NCBITAXID=43179;
 RN [1] SEQUENCE FROM N.A.
 RC TISSUE=Pancreas;
 RA TREUREA M.M., BUCK M.J., GUHANIYOGI J., SQUIRE T.L., ANDREWS M.T.;
 RT "Regulation of PDK4 expression in a hibernating mammal.;"
 RL Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
 CC -!- FUNCTION: Insulin decreases blood glucose concentration. It increases cell permeability to monosaccharides, amino acids and fatty acids. It accelerates glycolysis, the pentose phosphate cycle, and glycogen synthesis in liver.
 CC -!- SUBUNIT: Heterodimer of a B chain and an A chain linked by two disulfide bonds.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the insulin family.

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EMBL; AY038604; RAK72558.1; -.
 DR HSSP; P01308; IEG6.
 DR InterPro; IPR004825; Ins/IGF/relax.
 DR PF0049; Insulin; 1.
 DR PRINTS; PR00277; INSULINB.
 DR PRODOM; PDO15667; Mollusc_ins; 1.
 DR SMART; SM00078; ILGF; 1.
 DR PROSITE; PS00262; INSULIN; 1.
 DR KW Glucose metabolism; Hormone; Insulin family; Signal.
 FT SIGNAL 1 24 BY similarity.
 FT CHAIN 25 54 Insulin B chain.
 FT PROPEP 57 87 C peptide.
 FT CHAIN 90 110 Insulin A chain.
 FT DISULFID 31 96 Interchain (By similarity).
 FT DISULFID 43 109 Insulin B chain (By similarity).

RESULT 9

INS_CANFA STANDARD; PRT; 110 AA.

ID INS_CANFA 01321; 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Insulin precursor.
 GN Name=INS; Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OC NCBITAXID=9615;
 RN [1] SEQUENCE FROM N.A.
 RN MEDLINE=83109071; PubMed=6296142;
 RX Kwok S.C.M., Chan S.J., Steiner D.F.;
 RA Smith L.F.;
 RT "Cloning and nucleotide sequence analysis of the dog insulin gene. Coded amino acid sequence of canine preproinsulin predicts an additional C-peptide fragment.";
 RL J. Biol. Chem. 258:2357-2363 (1983).
 RN [2] SEQUENCE OF 25-54 AND 90-110.
 RX MEDLINE=66160119; PubMed=5949593; DOI=10.1016/0002-9343(66)90145-8;
 RA Smith L.F.;
 RT "Species variation in the amino acid sequence of insulin."
 RL Am. J. Med. 40:62-66 (1966).
 CC -!- FUNCTION: Insulin decreases blood glucose concentration. It increases cell permeability to monosaccharides, amino acids and fatty acids. It accelerates glycolysis, the pentose phosphate cycle, and glycogen synthesis in liver.
 CC -!- SUBUNIT: Heterodimer of a B chain and an A chain linked by two disulfide bonds.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the insulin family.

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 CC EMBL; V00179; CA33475.1; -.
 DR PIR; A92413; IPDG.
 DR PRINTS; PR01317; IAPH.
 DR InterPro; IPR004825; Ins/IGF/relax.
 DR PF00049; Insulin; 1.
 DR PRINTS; PR00277; INSULINB.
 DR PRODOM; PDO15667; Mollusc_ins; 1.
 DR SMART; SM00078; ILGF; 1.
 DR PROSITE; PS00262; INSULIN; 1.
 DR Direct protein sequencing; Glucose metabolism; Hormone; KW Insulin family; Signal.
 FT SIGNAL 1 24 Insulin B chain.

PT PROPEP 57 87 C peptide.
 PT CHAIN 90 110 Insulin A chain.
 PT DISULPID 31 96 Interchain.
 PT DISULFID 43 109 Interchain.
 PT DISULFID 95 100
 SQ SEQUENCE 110 AA; 12190 MW; A574791864A4FB98 CRC64;
 Query Match 78.6%; Score 404; DB 1; Length 110;
 Best Local Similarity 88.2%; Pred. No. 1; 2e-33; 1; Mismatches 11; Indels 0; Gaps 0;
 Matches 75; Conservative 1; MisMatches 9; Indels 0; Gaps 0;
 Qy 11 FVNQHLCGSHLVEALYLVCGERGFFYTPKVKRREADPQVQEVLEGGPGAGSISQPLALEC 70
 25 FVNQHLCGSHLVEALYLVCGERGFFYTPKVKRREADPQVQEVLEGGPGAGSISQPLALEC 70
 Db 71 SLOKGIVIVEQCTSTCSLYQLENYC 95
 Qy 71 SLOKGIVIVEQCTSTCSLYQLENYC 95
 Db 85 ALQKGIVIVEQCTSTCSLYQLENYC 109
 RESULT 10
 INS_HORSE STANDARD; PRT; 86 AA.
 AC POL10;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE insulin precursor;
 GN NamesINS;
 OS Equus caballus (Horse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perisodactyla; Equidae; Equus.
 OX NCBI_TaxID=9796;
 RN [1]
 RP SEQUENCE OF 1-30 AND 66-86.
 RX Published=J37344;
 RA Harris J.I.; Sanger F.; Naughton M.A.;
 RT "Species differences in insulin."
 RL Arch. Biochem. Biophys. 65:427-438(1956).
 RN [2]
 RP SEQUENCE OF 33-63.
 RX MEDLINE=73061498; PubMed=4640931;
 RA Tager H.S.; Steiner D.F.;
 RT "Primary structures of the proinsulin connecting peptides of the rat
 and the horse.";
 RL J. Biol. Chem. 247:7935-7940(1972).
 CC -!- FUNCTION: Insulin decreases blood glucose concentration. It
 increases cell permeability to monosaccharides, amino acids and
 fatty acids. It accelerates glycolysis, the pentose phosphate
 cycle, and glycogen synthesis in liver.
 CC -!- SUBUNIT: Heterodimer of a B chain and an A chain linked by two
 disulfide bonds.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the insulin family.
 CC residues assumed by homology to be present in the precursor
 molecule.
 DR PIR: A01580; IPHO.
 DR HSSP; P01317; IAPH.
 DR InterPro; IPR04825; Ins/IGF/relax.
 DR Pfam; PF0049; Insulin; 1.
 DR PRINTS; PR0277; INSULINB.
 DR SMART; SM00078; IIGF; 1.
 DR PROSITE; PS00262; INSULIN; 1.
 KW Direct Protein Sequencing; Glucose metabolism; Hormone;
 KW Insulin family.
 PT CHAIN 1 30 Insulin B chain.
 PT PROPEP 33 63 C peptide.
 PT CHAIN 66 86 Insulin A chain.
 PT DISULPID 7 72 Interchain.
 PT DISULFID 19 85 Interchain.
 PT DISULPID 71 76
 SQ SEQUENCE 86 AA; 9142 MW; A3E1E822711BDB46 CRC64;

RESULT 11
 INS_MOUSE STANDARD; PRT; 110 AA.
 ID _INS2_MOUSE STANDARD; PRT; 110 AA.
 AC P01326;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE insulin 2 precursor;
 GN Name=Ins2; Synonyms=Ins-2;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87163768; PubMed=3104603;
 RA Wentworth B.M.; Schaefer I.M.; Villa-Komaroff L.; Chirgwin J.M.;
 RT "Characterization of the two nonallelic genes encoding mouse
 RT proinsulin.";
 RL Mol. Evol. 23:305-312(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NON;
 RX MEDLINE=90372989; PubMed=23397023;
 RA Sawa T.; Ohgaku S.; Morioka H.; Yano S.;
 RT "Molecular cloning and DNA sequence analysis of preproinsulin genes in
 the NON mouse, an animal model of human non-obese, non-insulin-
 dependent diabetes mellitus";
 RL Mol. Endocrinol. 5:61-67(1990).
 RN [3]
 RP SEQUENCE OF 25-54 AND 90-110.
 RX MEDLINE=72189455; PubMed=5563718;
 RA Buenzl H.F.; Glüthhaar B.; Kunz P.; Muelhaupt E.; Humbel R.E.;
 RT "Amino acid sequence of the two insulins from mouse (*Maus musculus*).";
 RL Hoppe-Seyler S. Z. Physiol. Chem. 353:451-458(1972).
 CC -!- FUNCTION: Insulin decreases blood glucose concentration. It
 increases cell permeability to monosaccharides, amino acids and
 fatty acids. It accelerates glycolysis, the pentose phosphate
 cycle, and glycogen synthesis in liver.
 CC -!- SUBUNIT: Heterodimer of a B chain and an A chain linked by two
 disulfide bonds.
 CC -!- SIMILARITY: Belongs to the insulin family.
 CC -!- SUBCELLULAR LOCATION: Secreted.
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 or send an email to license@isb-sib.ch).
 CC
 DR EMBL; X04724; CA28433.1; -.
 DR PIR; A26342; INNS2.
 DR HSSP; P01317; IAPH.
 DR MGD; MGI:96573; Ins2.
 DR GO; GO:0005634; C:nucleus; IDA.
 DR GO; GO:0005732; C:small nucleolar ribonucleoprotein complex; IDA.
 DR GO; GO:0000187; P:activation of MAPK; IDA.

RESULT 13

INS_CRIGO	STANDARD;	PRT;	110 AA.		
ID	INS1_RAT	STANDARD;	PRT;	110 AA.	
AC	P01313;	STANDARD;	PRT;	110 AA.	
DT	21-JUL-1986 (Rel. 01, Created)	STANDARD;	PRT;	110 AA.	
DT	01-JAN-1990 (Rel. 13, Last sequence update)	STANDARD;	PRT;	110 AA.	
DE	Insulin precursor.	STANDARD;	PRT;	110 AA.	
GN	Name=INS;	STANDARD;	PRT;	110 AA.	
OS	Cricetulus longicaudatus (Long-tailed hamster) (Chinese hamster).	STANDARD;	PRT;	110 AA.	
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae; Cricetulus; Saccostomidae; Muridae; Murinae; Rattus norvegicus (Rat);	STANDARD;	PRT;	110 AA.	
OX	OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus norvegicus (Rat);	STANDARD;	PRT;	110 AA.
NCBI_TaxID	1030;	STANDARD;	PRT;	110 AA.	
RN	[1]	SEQUENCE FROM N.A.	STANDARD;	PRT;	110 AA.
RX	MEDLINE=B133036; PubMed=6365663;	STANDARD;	PRT;	110 AA.	
RT	"Sequence of a cDNA encoding Syrian hamster preproinsulin."	STANDARD;	PRT;	110 AA.	
RL	Diabetes 33:297-300(1984).	STANDARD;	PRT;	110 AA.	
RN	[2]	SEQUENCE OF 25-54 AND 90-110.	STANDARD;	PRT;	110 AA.
RA	Neelon F.A., Delcher H.K., Steinman H., Lebovitz H.E.;	STANDARD;	PRT;	110 AA.	
RL	Red. Proc. 32:300-300(1973).	STANDARD;	PRT;	110 AA.	
CC	-!- FUNCTION: Insulin decreases blood glucose concentration. It increases cell permeability to monosaccharides, amino acids and fatty acids. It accelerates glycolysis, the pentose phosphate cycle, and glycogen synthesis in liver.	STANDARD;	PRT;	110 AA.	
CC	-!- SUBUNIT: Heterodimer of a B chain and an A chain linked by two disulfide bonds.	STANDARD;	PRT;	110 AA.	
CC	-!- SUBCELLULAR LOCATION: Secreted.	STANDARD;	PRT;	110 AA.	
CC	-!- SIMILARITY: Belongs to the insulin family.	STANDARD;	PRT;	110 AA.	
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INS1_RAT	STANDARD;	PRT;	110 AA.		
ID	INS1_RAT	STANDARD;	PRT;	110 AA.	
AC	P01322;	STANDARD;	PRT;	110 AA.	
DT	21-JUL-1986 (Rel. 01, Created)	STANDARD;	PRT;	110 AA.	
DT	21-JUL-1986 (Rel. 01, Last sequence update)	STANDARD;	PRT;	110 AA.	
DE	Insulin precursor.	STANDARD;	PRT;	110 AA.	
GN	Name=INS1; Synonyms=Ins-1;	STANDARD;	PRT;	110 AA.	
OS	Rattus norvegicus (Rat);	STANDARD;	PRT;	110 AA.	
OC	Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus norvegicus (Rat);	STANDARD;	PRT;	110 AA.	
OX	OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus norvegicus (Rat);	STANDARD;	PRT;	110 AA.
NCBI_TaxID	10116;	STANDARD;	PRT;	110 AA.	
RN	[1]	SEQUENCE FROM N.A.	STANDARD;	PRT;	110 AA.
RX	MEDLINE=B004034; PubMed=498283; DOI=10.1016/0092-8674(79)90070-9;	STANDARD;	PRT;	110 AA.	
RA	Cordell B., Bell G.I., Tischer E., Denoto F.M., Ullrich A., Pickett R.L., Rutter W.J., Goodman H.M.;	STANDARD;	PRT;	110 AA.	
RT	"Isolation and characterization of a cloned rat insulin gene."	STANDARD;	PRT;	110 AA.	
RN	[2]	SEQUENCE FROM N.A.	STANDARD;	PRT;	110 AA.
RC	Strain=Sprague-Dawley; Tissue=Liver;	STANDARD;	PRT;	110 AA.	
RX	MEDLINE=B004035; PubMed=499284; DOI=10.1016/0092-8674(79)90071-0;	STANDARD;	PRT;	110 AA.	
RA	Lomedico P., Rosenthal N., Efstratiadis A., Gilbert W., Koldodner R., Tizard R.;	STANDARD;	PRT;	110 AA.	
RT	"The structure and evolution of the two nonallelic rat proproinsulin genes."	STANDARD;	PRT;	110 AA.	
RL	Cell 18:545-558 (1979).	STANDARD;	PRT;	110 AA.	
RN	[3]	SEQUENCE FROM N.A.	STANDARD;	PRT;	110 AA.
RX	MEDLINE=B0040379; PubMed=6249167;	STANDARD;	PRT;	110 AA.	
RA	Lomedico P.T., Rosenthal N., Koldodner R., Efstratiadis A., Gilbert W.;	STANDARD;	PRT;	110 AA.	
RT	"The structure of rat proproinsulin genes."	STANDARD;	PRT;	110 AA.	
RN	[4]	SEQUENCE OF 25-54 AND 90-110.	STANDARD;	PRT;	110 AA.
RX	MEDLINE=B0067613; PubMed=4311938;	STANDARD;	PRT;	110 AA.	
RA	Steiner D.F., Clark J.L., Nolan C., Rubenstein A.H., Margoliash E., Atten B., Oyer P.E.;	STANDARD;	PRT;	110 AA.	
RT	"Proinsulin and the biosynthesis of insulin."	STANDARD;	PRT;	110 AA.	
RL	Recent Prog. Horm. Res. 25:207-202(1969).	STANDARD;	PRT;	110 AA.	
RN	[5]	SEQUENCE OF 57-87.	STANDARD;	PRT;	110 AA.
RX	MEDLINE=B73061498; PubMed=4640931;	STANDARD;	PRT;	110 AA.	
RA	Tager H.S., Steiner D.F.;	STANDARD;	PRT;	110 AA.	
RT	"Primary structures of the proinsulin connecting peptides of the rat and the horse."	STANDARD;	PRT;	110 AA.	
RL	J. Biol. Chem. 247:7936-7940(1972).	STANDARD;	PRT;	110 AA.	
RN	[6]	SEQUENCE OF 57-87, AND REVISIONS.	STANDARD;	PRT;	110 AA.
RX	MEDLINE=B72177385; PubMed=4554104;	STANDARD;	PRT;	110 AA.	
RA	Markussen J., Sundby P.;	STANDARD;	PRT;	110 AA.	
RT	"Rat-proinsulin C-peptides: Amino-acid sequences."	STANDARD;	PRT;	110 AA.	
RL	Eur. J. Biochem. 25:153-162(1972).	STANDARD;	PRT;	110 AA.	
CC	-!- FUNCTION: Insulin decreases blood glucose concentration. It increases cell permeability to monosaccharides, amino acids and fatty acids. It accelerates glycolysis, the pentose phosphate cycle, and glycogen synthesis in liver.	STANDARD;	PRT;	110 AA.	
CC	-!- SUBUNIT: Heterodimer of a B chain and an A chain linked by two disulfide bonds.	STANDARD;	PRT;	110 AA.	
CC	-!- SUBCELLULAR LOCATION: Secreted.	STANDARD;	PRT;	110 AA.	
CC	-!- SIMILARITY: Belongs to the insulin family.	STANDARD;	PRT;	110 AA.	

DR EMBL; V01242; CAM24559_1; -.
 DR EMBL; J00747; AAA41442_1; -.
 DR EMBL; M25584; AAA41439_1; -.
 DR PIR; A30788; IPR01.
 DR HSSP; P01308; IATF.
 DR RGD; 2915; Insl1.
 DR InterPro; IPR004925; Ins/IGF/relax.
 DR Pfam; PF00049; Insulin_1.
 DR PRINTS; PR00277; INSULINB.
 DR Prodrom; PD015667; Mollusc_ins; 1.
 DR SMART; SW0078; IIGF_1.
 DR PROSITE; PS00262; INSULIN_1.
 DR KW Direct protein sequencing; Glucose metabolism; Hormone;
 KW Insulin family; Multigene family; Signal.
 FT SIGNAL 1 24
 FT CHAIN 25 54
 PROPEP 57 87
 FT PROPEP 57 87
 FT CHAIN 90 110
 DISULFID 31 96
 DISULFID 43 109
 FT DISULFID 95 100
 SQ SEQUENCE 110 AA; 12420 MW; 51D606DA54AE3533 CRC64;

Query Match 75.7%; Score 389; DB 1; Length 110;
 Best Local Similarity 84.7%; Pred. No. 4_3e-32;
 Matches 72; Conservativeness 4; Mismatches 9; Indels 0; Gaps 0;

QV 11 FVNQHLCSSHVLVERLYLVCGERGRPFYTKTRRAEDPGVQELGSGPAGASIQPLALEG 70
 Db 25 FVQHQHLCGPFLVERLYLVCGERGRPFYTKSRREVEDPGVQPLIGGPEASQIQLALEV 84
 QY 71 SLOQKRGIVTEQQCCSISLYQLENYC 95
 : |||||:|||||:|||||:|||||:
 Db 85 AROKRGIVDQCCSISLYQLENYC 109

RESULT 15

INS_PIG ID INSPIG STANDARD; PRT; 108 AA.
 AC P01315; Q9TQS5;
 DT 21-JUN-1986 (Rel. 01, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)

DE Insulin precursor.
 Name=INS; GN OS Sus scrofa (pig).
 OC Mammalia; Eutheria; Detartoiodactyla; Suiua; Suidae; Sus.
 OX NCBI_TAXID=9823;
 RN [1] SEQUENCE FROM N.A.
 RP RT Han X.-G., Tuch B.-E.;
 RA "Complete porcine preproinsulin cDNA sequence";
 RL Submitted (May-1998) to the EMBL/GenBank/DDBJ databases.
 RN [2] SEQUENCE FROM N.A.
 RP STRAIN=LARGE white;
 RC MEDLINE=22135958; PubMed=12140586; DOI=10.1007/s00335-001-3059-x;
 RA Amarger V., Nguen M., Laebe A.S., Braunschweig M., Nezer C.,
 Georges M., Andersson L.;
 RA "Comparative sequence analysis of the INS-IGF2-H19 gene cluster in pigs";
 RA Mamm. Genome 13:388-398 (2002).

RN [3] SEQUENCER OF 25-08.

RP MEDLINE=62826645; PubMed=5657053;

RA Chance R.E., Ellis R.M., Bromer W.W.;
 Chance R.E., Ellis R.M., Bromer W.W.;
 Science 161:165-167 (1968).
 [4] REVISITON TO 59.

RA Chance R.E.;
 RA Submitted (JUL-1970) to the PIR data bank.

RN [5] X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
 RP Blundell T.L., Dodson G.G., Hodgkin D., Mercola D.;
 RT "Insulin. The structure in the crystal and its reflection in chemistry and biology.>";
 RT Adv. Protein Chem. 26:279-402(1972).

RN [6] X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS).
 RP Isaacs N.W., Agarwal R.C.;
 RT "Experience with fast Fourier least squares in the refinement of the crystal structure of rhombohedral 2-zinc insulin at 1.5-A resolution.";
 RT Acta Crystallogr. A 34:782-791 (1978).

RN [7] X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS).
 RP Baker B.N., Blundell T.L., Cutfield J.F., Cutfield S.M., Dodson B.J., Dodson G.G., Crowfoot Hodgkin D.M., Hubbard R.E., Isaacs N.W., Reynolds C.D., Sakabe K., Sakabe N., Vijayan N.M.;
 RT "The structure of 22n pig insulin crystals at 1.5-A resolution.";
 RL Philos. Trans. R. Soc. Lond. B, Biol. Sci. 319:369-456 (1988).

RN [8] X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
 RX MEDLINE=912126280; PubMed=177633; DOI=10.1107/S0108768190009570;
 RA Balschmidt P., Hansen F.B., Dodson G., Koerber F.;
 RL "Structure of porcine insulin co-crystallized with clupeine Z.>";
 RL Acta Crystallogr. B 47:975-986 (1991).

RN [9] X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS).
 RX MEDLINE=91222450; PubMed=222410; DOI=10.1107/S0108768190009570;
 RA Badger J., Harris M.R., Reynolds C.D., Evans A.C., Dodson E.J., Dodson G.G., North A.C.T.;
 RT "Structure of the Dig insulin dimer in the cubic crystal.";
 RL Acta Crystallogr. B 47:127-136 (1991).

RN [10] X-RAY CRYSTALLOGRAPHY (1.65 ANGSTROMS).
 RX PubMed=15299880;
 RA Dia J.-S., Wan Z.-L., Chang W.-R., Liang D.-C.;
 RT "Structure of monomeric porcine DesB1-B2 despentapeptide (B26-B30) insulin at 1.65-A resolution.";
 RL Acta Crystallogr. D 53:507-512 (1997).

CC -1- FUNCTION: Insulin decreases blood glucose concentration. It increases cell permeability to monosaccharides, amino acids and fatty acids. It accelerates glycolysis, the pentose phosphate cycle, and glycogen synthesis in liver.

CC -1- SUBUNIT: Heterodimer of a B chain and an A chain linked by two disulfide bonds.

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- SIMILARITY: Belongs to the insulin family.

CC -1- DATABASE: NAME=Protein Spotlight; NOTE=Issue 9 of April 2001; WWW=<http://www.expasy.org/spotlight/articles/spotlight09.html>.

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CC EMBL; AR064555; AAC77920_1; ALT_INIT.

DR EMBL; AV044828; AAL69550_1; -.

DR FDB; IDEI; X-ray; A/C=88-108; B/D=25-54.

DR PDB; 1IZA; X-ray; A/C=88-108; B/D=25-54.

DR PDB; 1ZB; X-ray; A/C=88-108; B/D=25-54.

DR PDB; 1MPJ; X-ray; A/C=88-108; B/D=25-54.

DR PDB; 1SDB; X-ray; A=88-108; B=27-49.

DR PDB; 1WAV; X-ray; A/C/E/G/I/K=88-108; B/D/F/H/J/L=25-54.

DR PDB; 1ZEI; X-ray; A/B/C/D/E/F=25-108.

DR PDB; 1ZNI; X-ray; A/C-B8-108; B/D=25-54.

DR PDB; 2TCI; X-ray; A/C-B8-108; B/D=25-54.

DR PDB; 3INS; Neutron; A/C=88-108; B/D=25-54.

DR PDB; 3MTH; X-ray; A/C=88-108; B/D=25-54.

DR PDB; 4INS, X-ray; A/C=88-108, B/D=25-54.
 DR PDB; 6INS, X-ray; E/F=25-108.
 DR PDB; 7INS, X-ray; A/C/E=88-108, B/D/F=25-54.
 DR PDB; 9INS, X-ray; A=88-108, B=25-54.
 DR InterPro; IPR004825, Ins/IGF/Relax.
 DR PFam; PF00049, Insulin.
 DR PRINTS; PR00277, INSULINB.
 DR PRODom; PRO015667, Mollusc_inb; 1.
 DR SMART; SM00078, IIGF; 1.
 DR PROSITE; PS0062, INSULIN; 1.
 KW 3D-structure; Direct protein sequencing; Glucose metabolism; Hormone;
 KW Insulin family; Signal.
 PT SIGNAL 1 24
 PT CHAIN 25 54 Insulin B chain.
 PT PROPEP 57 85 C peptide.
 PT CHAIN 88 108 Insulin A chain.
 PT DISURPID 31 94 Intercchain.
 PT DISURPID 43 107 Interchain.
 PT DISURPID 93 98
 PT HELIX 26 46
 PT STRAND 48 48
 PT HELIX 89 94
 PT HELIX 100 106
 PT STRAND 107 107
 SQ SEQUENCE 108 AA; 11671 MW; CB4491Ba29850BBB CRC64;
 Query Match Similarity 75.3%; Score 387; DB 1; Length 108;
 Best Local Similarity 87.1%; Pred. No. 6.8e-32; Gaps 1;
 Matches 74; Conservative 1; Mismatches 8; Indels 2; Gaps 1;
 Qy 11 FVNQHICGSHIVEAHVLYVCGERGFPTPKARRAEDDPQVQVLEGGPGAGSLQPLALEG 70
 Db 25 FVNQHICGSHIVEAHVLYVCGERGFPTPKARRAENPQAGAVELGG--GLGGQLALAEQ 82
 Qy 71 SLOKRGIVEQCTSTCISLYQDENYC 95
 Db 83 PPQKRGIVEQCTSTCISLYQDENYC 107

Search completed: May 20, 2005, 00:38:50
 Job time : 176 secs

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